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OM nucleic - nucleic search, using sw model

Run on: November 26, 2003, 17:50:05 ; Search time 226 Seconds
(without alignments)
8319.877 Million cell updates/sec

Title: US-09-835-976B-15
Perfect score: 4260
Sequence: 1 tgaatagaagtattcttagt.....aaaaaaaaaaaaaaaaaaaaa 4260

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq: *
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5: /cgn2_6/ptodata/2/ina/PCITUS_COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1648.4	38.7	3722	4	US-09-016-434-1129
2	514.4	12.1	2384	1	US-07-688-352C-27
3	514.4	12.1	2384	2	US-08-474-379C-27
4	514.4	12.1	2384	3	US-09-146-249A-27
5	514.4	12.1	2384	3	US-08-206-188B-27
6	514.4	12.1	2384	5	PCT-US91-02714-25
7	226	5.3	227	4	US-09-016-434-294
8	136.4	3.2	254	4	US-09-016-434-464
9	123.4	2.9	235	4	US-09-016-434-614
10	116	2.7	231	4	US-09-016-434-475
11	110.2	2.6	236	4	US-09-016-434-371
12	92.6	2.2	4098	4	US-09-268-866-1
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18	39.4	0.9	2276	4	US-09-205-258-183
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20	39.2	0.9	289	3	US-09-244-796-17
21	38.8	0.9	441	4	US-09-601-537-10
22	38.8	0.9	1332	4	US-09-057-762-1
23	38.8	0.9	1332	3	US-08-326-119A-1
24	38.8	0.9	1493	6	5340934-5
25	38.8	0.9	4121	4	US-09-601-537-9
26	38.6	0.9	251	3	US-09-221-298-23
27	38.4	0.9	3527	2	US-08-909-965C-7

28	38	0.9	208	1	US-08-686-878A-37	Sequence 37, Appl
29	38	0.9	208	4	US-09-175-928-37	Sequence 37, Appl
30	37.8	0.9	1693	2	US-08-487-113D-118	Sequence 118, App
31	37.8	0.9	1693	2	US-08-720-420A-118	Sequence 118, App
32	37.8	0.9	2296	3	US-08-496-841C-137	Sequence 137, App
33	37.8	0.9	2634	2	US-08-818-514-1	Sequence 1, Appli
34	37.8	0.9	2634	2	US-08-818-514-2	Sequence 2, Appli
35	37.8	0.9	2634	3	US-09-115-934A-1	Sequence 1, Appli
36	37.8	0.9	2634	3	US-09-115-934A-2	Sequence 2, Appli
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38	37.8	0.9	2634	4	US-09-611-175-2	Sequence 2, Appli
39	37.4	0.9	1249	4	US-09-461-325-128	Sequence 128, App
40	37.4	0.9	1260	4	US-09-461-325-93	Sequence 93, Appl
41	37	0.9	2589	3	US-08-569-749-1	Sequence 1, Appli
42	37	0.9	2589	5	PCT-US96-12860-1	Sequence 1, Appli
43	36.8	0.9	1641	1	US-08-300-903A-8	Sequence 8, Appli
44	36.8	0.9	1641	4	US-08-988-197-8	Sequence 8, Appli
45	36.8	0.9	2434	4	US-09-489-847-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1
US-09-016-434-1129
; Sequence 1129, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1129:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3722 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1399211
US-09-016-434-1129
Query Match 38.7%; Score 1648.4; DB 4; Length 3722;
Best Local Similarity 71.1%; Pred. No. 0;

Matches 2196; Conservative 0; Mismatches 888; Indels 6; Gaps 1;			
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Qy	596	GAAGGTGCTTCCCTCCTCAACCGCATGGCCAAATACACTAATCTGACTCAAGGAGCAAA	655
Db	286	AAAGGTATCGTCTCTCTGGGAAAGCTGTCAGCTACACCACTCAACCGAGGGGCCAA	345
Qy	656	GGAACATGAAGGAGGAGCAAAAACATCACTGAAGGGGAAAGAGCCCAACAGACCCCA	715
Db	346	AGAGCATGAGGAGGCGAGAGTGGGAGGAGCCCGCGGAGGCGAGCGAGGCCACCCAG	405
Qy	716	AATGGTACCTTCATGGGTGCTACTCCCATGTCTACAAATATTTTGGAGTATGCT	775
Db	406	CATGGGCACTCATGGGGGTGACCTGCCCTGCCCTGCAGAAATATCTTTGGGGTATGCT	465
Qy	776	TTTTTTTACGCCCTTACATGGGTGGTGGGACAGCTGGAGTCTTTCAGGCTTTTGGCAATTGT	835
Db	466	CTTCCTCGCGCTACCTGGATGGTGGGCACAGAGGTGTCTACAGGCCCTCTCATCGT	525
Qy	836	CCTTATCTGCTGCTGTCTACAAATGTTGACTGCTATCTCCATGAGTGCCATTTGCCACTAA	895
Db	526	GCTTATCTGCTGTGTGTACCTGCTGACGGCCATCTCCATGAGTGCCATGCCACCAA	585
Qy	896	TGGAGTGGTCCAGCTGGGGGCTCACTTTATGATTTCCGGGCACTGGGCCAGAGTT	955
Db	586	CGGTGTGGTTCAGCTGGGGGCTCTATTTTCATGATCTCTGCTCACTGGGGCCAGAAAT	645
Qy	956	TGTTGGGGTGTGGGCTCTGCTTTTATCTTGGTACCACATTTGACAGGCCATGTACAT	1015
Db	646	TGGAGTGTGTGGGCTGTGCTTCTACCTGGGAACAACATTCGACGACGCCATGTACAT	705
Qy	1016	CCTGTGTGCATTAATAATCTTCTGTGCTATATGCTGCTGCTGCTGCTGCTGCTGCTGCT	1075
Db	706	CCTGGGGGCATCGAGATCTTGTGACCTTACATTTGCCACACAGCTGCCATTTTTTACCC	765
Qy	1076	TGATGAGGCACCTCAAGGAATCAGCAGCCATGTAAATACATCGCTGTCTAGGCACAGC	1135
Db	766	ATCGGTGTCTATGACACGTGGAATGCCACTTTTGAACAATATGCGTGTATGGGACCAT	825
Qy	1136	TTTCTTTGGTCTTATGGTATTTAGTGTATTTATGCGCGTACGCTATGTGAACAAGTTTGC	1195
Db	826	TTTCTTGAACCTTCATGACCTGTGTGTGTGTGGGGTCAAGTATGTGAACAAATTTGC	885
Qy	1196	CTCAATTTTCTGGCCTGTGTATGTCCTATGTCCTATGTCCTATGTCCTATGTCCTATGTC	1255
Db	886	CTCGCTCTTCTGGCCTGTGTATGTCCTATGTCCTATGTCCTATGTCCTATGTCCTATGTC	945
Qy	1256	GTCTTCTTTTGTCTCCACACTTCCGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1315
Db	946	GTCTATTTTGAACCTCCCGTGTTCCTGGTATGCTATGCTGGGCAACAGGACCTGTCCCG	1005
Qy	1316	AAGACACATTTGAGTGTCTTAAAGCAAGGAAATTAACAACATGACAGTCCCATCAAA	1375
Db	1006	GGACAGTTTATGATCTGTGCGCAAGACAGCTGTAGTGAGCAATGAGACAGTGGCCACCA	1065
Qy	1376	GTTATGGGAAATCTTCTGTAACCTGAGTCAATTTTTCATGTCACCTGTGATGAATATT	1435
Db	1066	GCTATGGAGTTTCTTCTGCGACAGCCCAACCTTACGACCGACTCTCTGTGACCCCTACTT	1125
Qy	1436	TGTTCAATAAGCTCACTTCAATCCAGGCACTTCTGGATTTGGCTAGTGGTATATTTAC	1495
Db	1126	CATGCTCAACAATGTGACCGAGATCCCTGGCATCCCGGGGAGCTGCTGGTGTGTCCA	1185
Qy	1496	AGAGAACTTTTGGAGTAAATTAACCTACCAAGGAGAGATCATCAAAAAGCTTTCAGCCAA	1555
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Qy	1610	CACCTCTTCAACGCTTCTGCTGGGAATCTTCTTCCCTCTGTTACAGGTATCATGGCTGG	1669
Db	1306	CACATCTTCAACGCTTCTGCTGGCACTTCTTCTTCCCTCTGTTAAACAGCATCATGGCTGG	1365
Qy	1670	ATCAACAGATCTGGAGATCTGAAGATGCTCAGAAATCTATTTCCGATTTGATGATATCT	1729
Db	1366	CTCAACCGCTCTGGGACCTTCTGAGCGCCAGAAATCTATCTCTGCTGGGAGCAATCT	1425
Qy	1730	TGCCATCTGACACCTCTTCTTATTTAAAGCAATGTTGCTCTTCTTCTTCTTCTTCTTCT	1789
Db	1426	GGCCATCATTTACAACTTCTCTGCTGCTATCTCAGCAGTGTGCTCTCTTCTTCTTCTTCT	1485
Qy	1790	TGAAGGGTGTCTCTCAGAGACAAATTCGGTGTGCTGTAAGAGGTAAATTTGGTGGTAGG	1849
Db	1486	TGAGGGTGTGCTCTCTCGGACAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1545
Qy	1850	CACCTTATCTTGGCCATCCCATGGGTGATTTGTTATTTGGCTCTTCTTCTTCTTCTTCTT	1909
Db	1546	CACATGCGCTGGGCTTCACTGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1605
Qy	1910	GGCTGGATTCAGAGCCTCAAGGTGACCGAGGCTGCTCAAGCTATTTGCAAGGATAA	1969
Db	1606	CGCTGGCTCCAGAGCCTCAAGGGGACCAAGGCTATTTGAGGCGCATTTGCCAAGGACAA	1665
Qy	1970	CATCATACCGTCTTCTGAGGGTCTTGGCCACAGCAAAAGCCAAATGGGAAACCTACCTGGGC	2029
Db	1666	CATCATCCCTCTCTCGGGTGTCTTGGCCACGGGAAGGTGAATGCTGTAACCCACATGGGC	1725
Qy	2030	TTTACTTCTAACTGCTGCCATTTGAGAGCTTTGGAATATCTCATTTGCTCTTCTTCTTCTT	2089
Db	1726	ACTCTCTGACGCACTCATCGCGAGCTGGGCACTCTCATCGCTCTCTCTCTCTCTCTCT	1785
Qy	2090	GGCCCCATCTTCTTCCATGTTTCTCATGTTTACCTCTTCTTCTTCTTCTTCTTCTTCTT	2149
Db	1786	GGCCCCATCTTCTTCCATGTTTCTCATGTTTACCTCTTCTTCTTCTTCTTCTTCTTCTT	1845
Qy	2150	CTTGCAACATTTACTTCGAACACCACTGAGAGACCCCGATTTCCGCTACTACCATTTGGGC	2209
Db	1846	GGTGAGACACTCTCTGAGACCCCACTGCGGCGCCGCTTCAAGTACTATCATCTGGGC	1905
Qy	2210	CCTTCTTCTTCAAGGATGATCTGCTGGCTCTGATGTTCAITTTCTTCTTCTTCTTCTTCTT	2269
Db	1906	GCTGCTCTCTGGCATGATCTCTGCTGGCTTATGTTGCTCTCTCTCTCTCTCTCTCTCT	1965
Qy	2270	TGCCATTTAGCCATGTAATAGTGTATGATCTCAAGTACATTTGAATACCAAGGAGC	2329
Db	1966	TGCCCTGGTGGCCATGCTCATCGCGGATGATCTTACAAATACATCGAGTACCAAGGGGC	2025
Qy	2330	TGAGAAAGATGGGTGATGTTATCCGTGGCTGTCTCTCAGTGCAGCCCGCTTGTCTTT	2389
Db	2026	TGAGNAGAGTGGGTGACGGGATCCGAGGCTGTCTCTGAGCGCTGCCCGCTACGCGCT	2085
Qy	2390	GCTTCGATTTGAGGAGGACCTCCACACATPAAAACTGGAGGCTCAGTGTCTTGTATT	2449
Db	2086	GTTGGGCTGGAGGAGGCGCTCTCTCACCAAGAACTGGCGGCGCAGCTGCTGCTGCT	2145
Qy	2450	ACTGAACTAGATGAACTTACATGTCAGACATCTCGCTCTCTCTCTCTCTCTCTCTCTCT	2509
Db	2146	GCTGAAGTGGACGAGGACCTCCAGTGAATCCCGCGGCTCTCTCTCTCTCTCTCTCTCTCT	2205
Qy	2510	GCTCAAGCAGGAAAGGTTTCACTATTGTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2569
Db	2206	GCTCAAGCTGGCAAGGCTGACCATTTGTTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2265
Qy	2570	GAACTACCGTGAAGTCTTGTGTGACAGACCAATAAGCACTTAATGGAGGAGAGAA	2629
Db	2266	GAGCTATGGCGAGGCTCAGGCGCGGAGACCATCAAGAACATGATGGAATTTGAGAA	2325
Qy	2630	GCTAAAGGATCTCCAGCTGGTGGCGCCAGCTGAGAGGAGGCTTTTCCACCT	2689
Db	2326	GGTGAAGGGCTTCTCCAGGCTGGTGGCCAGCAAGGTGGGGAGGGGCTGGCCACCT	2385

Db	597	CGGTGTGGTTCAGCTGGGGGCTCCTATTTCATGATCTCTCGTTCACTGGGGCCAGAAATT	556
Qy	956	TGTTGGGGCTGTGGGCTCTGCTTTTATCTTGGTACCACATTTGCAGCAGCCATGTACAT	1015
Db	657	TGGAGTGTCTGTGGGCTGTGCTTCTACCTGGGAACAACATTCGACGACCCATGTACAT	716
Qy	1016	CCTTGGTGCCATTTGAATCTTTCTGTGCTATATCTGTCCCGCAGAGCTGCCATCTTTCACAG	1075
Db	717	CCGTGGGGCCATCGAGATCTTGTGACCTACATTGCCCCACCAAGCTGCCATTTTTTACCC	776
Qy	1076	TGATGCGCACTCAAGGAATCAGCAGCCATGCTAAATAACATCGCTGTCTACGGCACAGC	1135
Db	777	ATCGGGTCTCATGACACGTCGAATGCCACTTTGAACAATATCGGTGTGTATGGGACCAT	836
Qy	1136	TTTCTTGGTCCCTTATGGTATTAGTGGTATTTATCGGCGTACGCTATGTGAACAAGTTTGC	1195
Db	837	TTTCTGGCCTTCATGACCCCTGGTGGTGTGTGGGGTCAAGTATGTGAACAAATTTGC	896
Qy	1196	CTCANTTTTCTGGCCTGTGTCAATGTGTCCATCTTGGCCATCTATGCTGGAGCCATCAA	1255
Db	897	CTCGCTTCTCTGGCCTGTGTGATCACTCCATCCTCTCCATCTATGCTGGGGGCATAAA	956
Qy	1256	GTCTTCTTTTGTCTCTCCACACTTCCGGGTCTGCATGCTGGGTAAACGCACTCTTTTCATC	1315
Db	957	GTCTATATTGTACCCCTCCGTGTTCCGGTATGATGCTGGGCAACAGGACCTGTGCCG	1016
Qy	1316	AAGACACATTGACGTTTGTCTTAAGACCAAGGAAATTAACAACATGACAGTCCCACAAA	1375
Db	1017	GGACCAGTTTGAACATCTGTGCCAAGACAGCTGTAGTGGAACAATGAGACAGTGCCACCCA	1076
Qy	1376	GTTATGGGATTTCTTGTAACTCGAGTCAATTTTTCATGCCACCTGTGATGAATACTT	1435
Db	1077	GCTATGAGATTCTTTGSCACAGCCCAACCTTAACACGATCTCTGTGACCCCTACTT	1136
Qy	1436	TGTTCAACATAACGTCACTTCAATCCAGGCGATTCTGTGATTGGCTAGTGGTATAATTAC	1495
Db	1137	CATGCTCAACAAATGTGACCGAGATCCCTGGCATCCCGGGCAGCTGCTGGTGTCTCCA	1196
Qy	1496	AGAAATCTTTGGAGTAATTACTCTCAAGGAGGAGATCATCGAAAGCCTTCAGCCAA	1555
Db	1197	GGAAAACTGTGGAGCCCTACCTGGAGAAGGGTGACATCGTGAGAAGCATGGGCTGCC	1256
Qy	1556	ATCTTCTGTGATCTTAGGCACTTAA-----CCATGAATATGTTCTTCTTCACATCAC	1609
Db	1257	CTCGCAGATGCCCGGACGCTGAAGGAGAGCGTCTCTGTAGTGGTGCCTGACATCGC	1316
Qy	1610	CACCTCCTTCACGCTTCTGGTGGGAATCTTCTTTCCCTCTGTTCACAGTATCATGGCTGG	1669
Db	1317	CACATCCTTCACGCTGTGTGTGCGCATCTTCTTCTTCTTCTGTAAAGTATGGCATGGT	1376
Qy	1670	ATCAACAGATCTGG	1684
Db	1377	GTACAGGAACTTG	1391

RESULT 3

776	TTTTTTACGCCTTACATGGGTGGGACAGCTGGAGTTCCTCAGGCTTTTGC	835
QY	US-08-474-379C-27	
	Sequence 27, Application US/08474379C	
	Patent No. 5977305	
	GENERAL INFORMATION:	
	APPLICANT: Wigler, Michael H.	
	APPLICANT: Colicelli, John J.	
	TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED	
	TITLE OF INVENTION: PROCESSES	
	NUMBER OF SEQUENCES: 88	
	CORRESPONDENCE ADDRESS:	
	ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun	
	STREET: 233 South Wacker Drive/6300 Sears Tower	
	CITY: Chicago	
	STATE: Illinois	
	COUNTRY: United States of America	
	ZIP: 60606-6402	
	COMPUTER READABLE FORM:	
477	CTTCTCGCGGTGACCTGGATGGTGGGACAGCAGAGGTGTGCTACAGGCCCTCTC	536
Db		
836	CCTTATCTGCTGCTGCTCAAAATGTTGACTGTCTATCTCCATGAGTGCCCAT	895
QY		
537	GCTTATCTGCTGCTGTTGTTACCTGCTGACGGCCATCTCCATGAGTGCCCAT	596
Db		
896	TGGAGTGGTGGCAGCTGGGGCTCATACTTTATGATTTCCCGGCACCTGGGCC	955
QY		
597	CGGTGTGGTTCAGCTGGGGGCTCCTATTTCAATGATCTCTCGTTCACTGGGG	656
Db		
956	TGGTGGGGCTGTTGGCCTCTGCTTTTATCTTGTTACCAATTTGCACAGCCCAT	1015
QY		
657	TGGAGTGTCTGGGGCCTGTGCTCTACCTGGGAAACAATTTGCACAGCCCAT	716
Db		
1016	CCTTGGTGCATTTGAAATCTTTTCTGGTCTATATCGTCCCCCGAGCTGCCAT	1075
QY		

Db	717	CTGGGGCCATGAGATCTTGTGACCTACATTGGCCCCACCAGCTGCCATTTTTTATCCC	776
Qy	1076	TGATGACGCACTCAAGGAATCAGCAGGCCATCTAAATAAACATGCGTGTCTACGGCAGCAGC	1135
Db	777	ATCGGGTGCTCATGACACGTCGAATGCCACTTTGAACAATATGCGTGTATGGACCAT	836
Qy	1136	TTTCTTGGTCTTAATGATATTAGTGGTATTTATCGGCGTAGCGTATGTGAACAAGTTTGC	1195
Db	837	TTTCTCGGCTTTCATGACCCCTGGTGGTGTGTTGTGGGGTCAAGTATGTGAACAAATTTGC	896
Qy	1196	CTCANTTTTCTGCGCTGTGTCATTTGTGTCATCTTGGCCATCTATGCTGGAGCCATCAA	1255
Db	897	CTCGCTCTTCTGCGCTGTGTGATCATCTCCATCCTCTCCATCTATGCTGGGGGCATAAA	956
Qy	1256	GTCTTTCTTTTGTCTCTCCACACTTCCCGGTCTGCATGCTGGGTAAACCGCACTCTTTTCATC	1315
Db	957	GTCTATATTGACCTCCCGTGTTCGGGTATGATGCTGGGCAACAGGACCTGTGCCG	1016
Qy	1316	AAGACATTTGACCTTTGTCTTAAGACCAAGGAATTAACAACATGACAGTCCCATCAA	1375
Db	1017	GGACAGTTTTGACATCTGTGCAAGACAGCTGTAGTGGACAAATGAGACAGTGGCCACCA	1076
Qy	1376	GTTATGGGATCTTCTGTAACTCGAGTCAATTTTTCAATGCCACCTGTGATGAATCTT	1435
Db	1077	GCTATGAGATTCTTCTGCCACAGCCCAACCTTAACACCGACTCTGTGACCCCTACTT	1136
Qy	1436	TGTTCAACAATAACGTCACTTCAATCCAGGGCATTCCTGGATTGGCTAGTGGTATAATTAC	1495
Db	1137	CATGCTCAACAAATGTGACCGAGATCCCTGGCATCCCGGGGCGAGCTGCTGGTGTCTCA	1196
Qy	1496	AGAGATCTTTGGAGTAATTACTTACCCAGGGAGAGATCATCGAAAGCCTTCAGCCAA	1555
Db	1197	GGAAACCTCTGGAGCGCTACCTGGAGAAGGGTGACATCGTGAGAAGCATGGGTGCC	1256
Qy	1556	ATCTTCATGATCTTATGGCAGCTTAA-----CCATGAATATGTTCTTGTTCACATCAC	1609
Db	1257	CTCGCAGATGCCCGGACCTGGAAGAGAGCGCTGCTCTGTAGCTGGTGCCTGACATCGC	1316
Qy	1610	CACCTCCTTCCACGCTTCTGGTGGGAATCTTCTTTCCCTCTGTACAGGTATCATGGCTGG	1669
Db	1317	CACATCCTTCAACCGTGTGTGGCATCTTCTTCCCTTCTGTAAACGATTATGGCGATGGT	1376
Qy	1670	ATCAACAGATCTGG	1684
Db	1377	GTCAAGCAAGCAATTG	1391

RESULT 4

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US-09-146-249A-27
; Sequence 27, Application US/09146249A
; Patent No. 6069240
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/146.249A
; FILING DATE:

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Db 897 CTCGCTTCTCGGCTGTGTGATCATCTCCATCTCTCCATCTATGCTGGGGCATAAA 956
QY 1256 GTCTTCTTTTGTCTCCACACTTCCGGTCTGCTGCTGGTAAACCGACCTTTTTCATC 1315
Db 957 GTCTATATTTGACCTTCCGCTGTTCCGGTATGCTGCTGGCAACAGGACCTGTCCGG 1016
QY 1316 AAGACACATTTGCTGCTTAAGACCAAGGAAATTAACAACATGACAGTCCCATCAA 1375
Db 1017 GGACCAATTTGACATCTGTGCAAGACAGCTGTAGTGGACAATGAGACAGTGGCCACCA 1076
QY 1376 GTATGGGATTTCTTCTGTAACCTGAGTCAATTTTCAATGGCACTGTGATGAATATT 1435
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QY 1436 TGTTCACATAGCTCACATTCATCCAGGCAATCTCTGATTTGGTGTGATTAATTAC 1495
Db 1137 CATGCTCAACATGTGACGAGATCTCTGGCATCCCGGGGAGCTGTGGTGTGCTCA 1196
QY 1496 AGAATCTTTTGGAGTAATTACCTACCAAGGAGAGATCATCGAAAGCCTTCAGCCAA 1555
Db 1197 GGAAACCTGTGGAGCCTACCTGGAGAGGCTGACATCGTGGAGACATGGGCTGCC 1256
QY 1556 ATCTTCTGATGCTTAGGAGCTTAAA-----CATGAATATGTTCTTTGTGACATCA 1609
Db 1257 CTCGGAGATGCCCCAGGCTGAAAGAGAGCCTGCTCTGTAGTGTGCTGACATCGC 1316
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Db 1317 CACATCTTACCGTCTGTGCGCATCTTCTTCCCTTCTGTAACAGGTATGGCATGT 1376
QY 1670 ATCAACAGATCTGG 1684
Db 1377 GTCAGCAGAACTTG 1391

RESULT 5

US-08-206-188B-27
; Sequence 27, Application US/08206188B
; Patent No. 6100025
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,188B
; FILING DATE: 01-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 2384 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..1539, 1859..2383)
US-08-206-188B-27

Query Match 12.1%; Score 514.4; DB 3; Length 2384;
Best Local Similarity 66.0%; Pred. No. 3.6e-148;
Matches 762; Conservative 0; Mismatches 387; Indels 6; Gaps 1;

QY 536 AGGAGATGAATATTTTGTATATAAATTTGGCACTCTTTGAGGAAGAAATGGACACAGACC 595
Db 237 AGGAATTGACTATATGACAGAACTTGGCACTGTTTGGAGGAGAGCTGGACATCCGCC 296
QY 596 GAAGGTGTCTTTCCCTCTCAACCGCATGGCCAAATTTACACTAATCTGACTCAAGGAGCAA 655
Db 297 AAAGTATCTGCTCTTCTGGGAAAGCTCGTCAGCTACACCAACCTCACCCAGGCGCCAA 356
QY 656 GGAACATGAAGAGGAGAGAAACATCATGAAGGAAAGAAAGCCACCAAGACCCCA 715
Db 357 AGAGCATGAGGAGGCGGAGAGTGGGGAGGCAACCCCGGAGGCGAGCCGAGGCCACCCAG 416
QY 716 AATGGTATCTTCAATGGGTGTCTACCTCCCATGTCTACAAAATATTTTGGAGTGTACT 775
Db 417 CATGGCAACCTCATGGGGTGTACCTGCCCTGCTGCGAGAAATATCTTTGGGGTATCTCT 476
QY 776 TTTTTCACGCTTACATGGGTGGTGGGACAGCTGGAGTCTTTCAGGCTTTTGGCAATGT 835
Db 477 CTTCCTGGGCTGACCTGGATGGTGGGACAGCAGGTGTGCTACAGGCGCTCTCTCATCT 536
QY 836 CTTATCTGCTGCTGTACAAATGTTGACTGTCTATCTCCATGAGTGCATGGCACTAA 895
Db 537 GCTTATCTGCTGTGTGTACCTCTGACGGCCATCTCCATGAGTGCATTCGCCACCAA 596
QY 896 TGGAGTGTGCGAGCTGGGGCTCATCTTATGATTTCCCGGACACTGGGCCCAAGATT 955
Db 597 CGGTGTGTTCCAGCTGGGGCTCTTATTCATGATCTCTGTTCACTTGGGGCAGAAAT 656
QY 956 TGGTGGGCTGTGGCCCTCTCTTTTATCTTGTACCAACATTTGAGCAGGCAATGTACAT 1015
Db 657 TGGAGTGTCTGTGGGCTGTGCTTCTACCTGGAAACAACTTGGCAGCAGCATGTACAT 716
QY 1016 CTTGTGTCCTAATGAATCTTCTGGTCTATATGTCCTCCCGAGCTGCATCTTTCACAG 1075
Db 717 CTTGGGGCCATCGAGATCTTGTGACCTACATTTGCCCCACAGCTGCCATTTTTCACC 776
QY 1076 TGATGACGCACTCAAGGAATCAGAGCCATGCTAAATAACATGCTGTCTAGGCGACAGC 1135
Db 777 ATCGGGTCTCATGACACGTCGAATGCCACTTTGNAACAATATGCTGTGTATGGACCAT 836
QY 1136 TTTCTTGTCTCTATGATGATTTAGTGTATTTATCGGCTAGCTATGTGAACAAGTTTGC 1195
Db 837 TTTCTGTGCTTCAAGACCTGCTGTGTTTGTGGGGTCAAGTATGTGAACAATTTGC 896
QY 1196 CTCANTTTTCTGGCCTGTGTCATTTGTGTCATCTTGGCCATCTATGCTGGAGCCATCA 1255
Db 897 CTCGCTCTTCTGGCCTGTGTGATCATCTCCATCTCTTCCATCTATGCTGGGGCATAAA 956
QY 1256 GTCTTCTTTTGTCTCCACACTTCCCGTCTGCACTGCTGGTAAACCGCACTCTTTTCATC 1315
Db 957 GTCTATATTTGACCTCCCGTGTTCGGGTATGCAATGCTGGCAACAGGACCTGTCCCG 1016
QY 1316 AAGACACATTTGACGTTTGTCTTAAGACCAAGGAAATTAACAACATGACAGTCCCATCAA 1375
Db 1017 GGACCAATTTGACATCTGTGCAAGACAGCTGTAGTGGACAATGAGACAGTGGCCACCA 1076
QY 1376 GTTATGGGATTTCTTCTGTAACCTGAGTCAATTTTCAATGCCACTGTGATGAATATT 1435
Db 1077 GCTATGGAGTTTCTTCTGCAACAGCCCAACCTTACGACCGACTCTGTGACCCCTACT 1136

QY 1436 TGTTTCAATACGTCACCTTCAATCCAGGGGCAATTCCTGATGGCTAGTGGTATTAATTAC 1495
Db 1137 CATGCTCAACAATGTGACCGAGATCCCTGGCATCCCGGGGAGCTGCTGGTGTCTCCA 1196
QY 1496 AGAGAATCTTTGGAGTAAATTACTACCCAAAGGAGAGATCATCGAAAGCCTTCAGCCAA 1555
Db 1197 GGAAACCTGTGAGCGCTACTCGGAGAGGAGTGCATCGTGGAGAGCATGGGCTGCC 1256
QY 1556 ATCTTCTGATGCTTAGGAGCTTAAA-----CCATGAATATGTTTGTGACATCAC 1609
Db 1257 CTCGAGATGCCCGAGCCTGAAGAGAGCGCTGCTCTGTACGTGGTGGCTGACATCGC 1316
QY 1610 CACCTCCTTACGCTTCTGGTGGGAATCTTCTTCCCTCTGTTACAGGTATCATGGCTGG 1669
Db 1317 CACATCCTTCAACCGTGTGTCGGCATCTTCTTCCCTTCTGTAACAGGTATGGCGATGCT 1376
QY 1670 ATCAAAACAGATCTGG 1684
Db 1377 GTCAGCAGGAACCTTG 1391

RESULT 6

PCT-US91-02714-25

; Sequence 25, Application PC/TUS9102714

; GENERAL INFORMATION:

; APPLICANT: Wigler, Michael H.

; APPLICANT: Colicelli, John J.

; TITLE OF INVENTION: Cloning by Complementation and Related

; TITLE OF INVENTION: Processes

; NUMBER OF SEQUENCES: 55

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

; ADDRESSEE: Bicknell

; STREET: Two First National Plaza, 20 South Clark

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60603

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US91/02714

; FILING DATE: 19910419

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/511,715

; FILING DATE: 20-APR-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Borun, Michael F.

; REGISTRATION NUMBER: 25447

; REFERENCE/DOCKET NUMBER: 27805/30197

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 346-5750

; TELEFAX: (312) 984-9740

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2384 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1541

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1859..2383

PCT-US91-02714-25

Query Match 12.1%; Score 514.4; DB 5; Length 2384;

Best Local Similarity 66.0%; Pred. No. 3.6e-148;

Matches 762; Conservative 0; Mismatches 387; Indels 6; Gaps 1;

QY 536 AGGAGATCAATATTTTGATAAATAATTTGGCACTCTTTGAGGAGAAATGGACACCAGACC 595
Db 237 AGGAATTGACTACTATGACAGAAACCTGGCACTGTTTGAGGAAGAGCTGGACATCCGCC 296
QY 596 GAAGGTGCTTCCCTCCCTCAACCGCATGGCCAAATTAACACTAATCTGACTCAAGAGAGCAA 655
Db 297 AAAGTATGCTCTCTTCTGGGAAGAGCTGCTAGCTACACCAACCTCACCCAGGGGCCAA 356
QY 656 GGAACATGAAGAGCAGAAAAATCACTGAAGGAAAAAGAACGCCAACCAAGACCCCCCA 715
Db 357 AGAGCATGAGGAGCGGAGAGTGGGGAGGCGACCGCGGAGGGGAGCCGAGGACCCAG 416
QY 716 AATGGGTACCTTCATGGGTGCTACCTCCCATGCTACAAAATATTTTGGAGTGATCCT 775
Db 417 CATGGGCACCTCATGGGGGTGTACCTGCCCTCGCAGAAATATCTTTGGGGTTATCCT 476
QY 776 TTTTTCACGCTTACATGGGTGGGCGACAGCTGGAGTCTTTCAGGCTTTTTCACAAATGT 835
Db 477 CTTCTCGGGGTGACCTGGATGGTGGGCGACAGAGTGTGTACAGGCCCTCCTCATGCT 536
QY 836 CTTATCTGCTGCTGTACAAATTTTGACTGTCTATCTCCATGAGTGCCATTTGCCACTAA 895
Db 537 GCTTATCTGCTGCTGTGTACCTGCTGACGCCCATCTCCATGAGTGCCATGCCACCAA 596
QY 896 TGGAGTGTGCCAGCTGGGGCTCATCTTTATGATTTCCGGGGACCTGGGGCCAGAGTT 955
Db 597 CGGTGTGGTTCAGCTGGGGCTCCTATTTTCATGATCTCTGTTCACTGGGGCCAGAAAT 656
QY 956 TGGTGGGCTGCTGGCCCTCTCTTTATCTTGTGTACCAATTTGCGAGAGCCATGACAT 1015
Db 657 TGGAGTGTCTGTGGCCCTGCTTCTACCTGGGAACAAATTCGAGCAGCCATGATGAT 716
QY 1016 CTTTGTGCCATGAAATCTTCTGGTCTATATCTGCCCGAGCTGCCATCTTTTCACAG 1075
Db 717 CTTGGGGCCATCGAGATCTTGTGACCTACATATGCCCCACCCAGCTGCCATTTTACCC 776
QY 1076 TGATGAGCACTCAAGNAATCAGCAGCCATCTTAATAACATGCGTGTCTACGGCAGC 1135
Db 777 ATCGGGTGTCTATGACAGCTCGAATGCGACCTTTTGAACAATATGCGTGTGTATGGACCAT 836
QY 1136 TTTCTTGTCTTATGTTAGTGTATTTATCGGGTACGCTATGTGAACAAGTTTTC 1195
Db 837 TTTCTGGCCTTCATGACCTCCCTGGTGGTGTGTGGGGTCAAGTATGTGAACAATTTTC 896
QY 1196 CTCANTTTTCTGGCCTGTGTCTATTTGTCTCATCTTGGCCATCTATGCTGGAGCCATCAA 1255
Db 897 CTCGCTCTTCTGGCCTGTGTGATCACTCATCTCTCCATCTATGCTGGGGGATAAA 956
QY 1256 GTCCTTCTTGTCTCTCCACACTTCCCGGTCTGCATGCTGGGTAAACCCACTCTTTTTCATC 1315
Db 957 GTCTATATTTGACCTCTCCGCTGTTTCCGGTATGATGCTGGGCAACAGGACCTCTGCCG 1016
QY 1316 AAGACACATTTGACCTTCTCTAAGCAAGAAATTAACACATGACAGTCCCATCAA 1375
Db 1017 GGACCACTTTGACATCTGTGCAAGACAGCTGTATGTGGCAATGAGACAGTGGCCACCA 1076
QY 1376 GTTATGGGATTTCTTCTGTAACCTCGAGTCAATTTTCAATGCCACTCTGTGATGAATCTT 1435
Db 1077 GCTATGGAGTTTCTTCTGCCACAGCCCCAACCTTACGACCGACTCTCTGTGACCCCTACTT 1136
QY 1436 TGTTCAAAATACCTCACTTCAATCCAGGGCAATCTCTGGATTTGGTGTGTTAATTAAC 1495
Db 1137 CATGCTCAACAAATGTGACCGAGATCCCTGGCATCCCGGGGAGCTGTGTTGGTGTCTCCA 1196
QY 1496 AGAAGATCTTTGGAGTAAATTAACCTACCCNAGGGAGAGATCATCGAAAGCCCTTCAGCCA 1555
Db 1197 GGAAACCTGTGGAGCGCCTACCTGGAGAGGGGTGACATCTGTGGAGAGCATGGGCTGCC 1256

QY 1556 ATCTTCTGATGCTTTAGGAGCTTAA-----CCATGAATATGTTCTTGTGACATCAC 1609
Db 1257 CTCGGAGATGCCGAGCCTGAAGGAGAGCTGCTCTGTACGTGGTCGCTGACATGCC 1316
QY 1610 CACCTCCTTACGCTTCTGTGGGAATCTTCTTCCCTCTGTACAGGTATCATGGCTGG 1669
Db 1317 CACATCCTTACCGTGCTGTGCGCATCTTCTTCCCTCTGTAAACAGGTATGGCGATGGT 1376
QY 1670 ATCAACAGATCTGG 1684
Db 1377 GTCAGCAGGAAGTTG 1391

RESULT 7

US-09-016-434-294
; Sequence 294, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 294:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LIVRUT01
; CLONE: 1755202
US-09-016-434-294

Query Match 5.3%; Score 226; DB 4; Length 227;
Best Local Similarity 99.6%; Pred. No. 1.1e-59;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2864 CAGCAATGTGAGCAATTTTCTGAGGCAACATTGATGTGTGGTATGTGATGATGG 2923
Db 1 CAGCAATGTGAGCAATTTTCTGAGGCAACATTGATGTGTGGTATGTGATGATGG 60
QY 2924 GGGGATGCTTATGCTACTACCATCTCTGAAACAGCAACAGGTGTGGCGAAAGTCAG 2983
Db 61 GGGGATGCTTATGCTACTACCATCTCTGAAACAGCAACAGGTGTGGCGAAAGTCAG 120

QY 2984 CATACGGATCTTACAGTAGCCCAATTAGAAGACAACAGATATCCAAATGAAGAGGACCT 3043
Db 121 CATACGGATCTTACAGTAGCCCAATTAGAAGACAACAGATATCCAAATGAAGAGGACCT 180
QY 3044 AGCCACCTTCTATATACCTTACCGATTTAGGCGGAGGTAGAGTGG 3090
Db 181 AGCCACCTTCTATATACCTTACCGATTTAGGCGGAGGTAGAGTGG 227

RESULT 8

US-09-016-434-464
; Sequence 464, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 464:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSN0T16
; CLONE: 2233388
US-09-016-434-464

Query Match 3.2%; Score 136.4; DB 4; Length 254;
Best Local Similarity 74.6%; Pred. No. 6.1e-32;
Matches 170; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
QY 3390 CCGGACCACTCCAAATGTGAGCGGATGCATACAGCAGTGAAACTCAACGAGGTATAGTT 3449
Db 5 CCGGACCACTCCAAATGTGAGCGGATGCACACGGTGTGAAGCTCAATGGCGTCTGCTC 64
QY 3450 AACAAAGTCCCATGAAGCAAGCTGGTTTATTGAATATGCCAGGCGCACCCGAAACCT 3509
Db 65 AACAAAGTCCCATGAAGCTGGTTTATTGAATATGCCAGGCGCACCCGAAACCT 124
QY 3510 GAGGAGTGAAGAACTACATGAGGTCTCTAGAGGTCTCTACCGAGGACTAGAGGAGTC 3569
Db 125 CAGGAGAGCAGAGAACTACATGAGGTCTCTTGAAGTCTCTACCGAGGCGTGAACAGATC 184

[illegible]

RESULT 9

US-09-016-434-614
; Sequence 614, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Sailhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 614:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: CONUTUT01
; CLONE: 2508812
US-09-016-434-614

Query Match	2.9%	Score 123.4	DB 4	Length 235
Best Local Similarity	72.4%	Prsd. No. 6.1e-28		
Matches 160	Conservative 0	Mismatches 61	Indels 0	Gaps 0
QY	3012	GAAGACAAACAGTATCCAAATGAAGAGGAGCTAGCCACCTTCCTATATCACTTACGATT	3071	
DB	2	GAGCAGACAGCATCCAGATGAGAGGAGCTGCAGATGTTCTTGATCACTTCGGCATC	61	
QY	3072	GAGCGGAGGTAGAGTGGTGGAGATGCATGCACAGTGATATATCAGCATATACTTACGAG	3131	
DB	62	AGCGCCGAGTGGAGGTGGTGGAGATGGTTGAAAAAGACATATCTGCTTTCACCTACGAG	121	
QY	3132	CGCACTTTGATGATGGAACAAAGCTCCAGATGCTTCGGCAGATCGCGCTATCCAAACA	3191	
DB	122	AGGACACTAATGATGGAGCAGAGTCCAGATGCTGAAGCAGATGCAGCTGTCCAGAAC	181	
QY	3192	GAGCGAGACAGAGGAGCAATTTGGTGAAGAGCCGAAACTC	3232	
DB	182	GAGCAGAGGCGAGGCGCCAGCTGATCCAGCAGGGAACAC	222	

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Query Match	2.7%	Score 116;	DB 4;	Length 231;
Best Local Similarity	68.4%;	Pred. No. 1.2e-25;		
Matches 158;	Conservative 0;	Mismatches 73;	Indels 0;	Gaps 0;
Qy	2341	GGGGTGATGGTATCCGTGGGCTGCTCCCTCAGTGCAGCCCGGTTTGCTTTGCTTCGATTGG	2400	
Db	1	GGGGCGATGGCATCCGTGGCTATCCTGNA CGCCGCCGCTACGCCCTGCTCGCGGTGG	60	
Qy	2401	AGGAAGACCTCCACACACTAAAACTGAGGGCTCAGTTGTTGTTATTACTGAAACTAG	2460	
Db	61	AGCACGGTCCCCCCCACCAAGAACTGGAGGGCCCCAGGTGCTGTTGATGCTGTAACCTGG	120	
Qy	2461	ATCAAGACTTTACATGTCAAGCATCCTCGGCTCCTCACCCTTTGCTCCTCACAGCTCAAAAGCAG	2520	
Db	121	ACGGGNAACAGGCGGTGAAGACCCCGCTGCTGCTTTACGNCGCGAGCTGAAGCCG	180	
Qy	2521	GAAGAAGTNTCACTATTGTGGGCTGTGTATCGTGGGGAATTCCTAGAGA	2571	
Db	181	GCAAAGGCTTGACCATCTGTGGGTCGGTGGTTGGANGGACCGTACTTGGACA	231	

RESULT 11
US-09-016-434-371

; Sequence 371, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 371:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BEPINOT01
; CLONE: 2056018
; US-09-016-434-371

Query Match 2.6%; Score 110.2; DB 4; Length 236;
Best Local Similarity 66.8%; Pred. No. 7.4e-24;
Matches 157; Conservative 0; Mismatches 78; Indels 0; Gaps 0;
QY 2667 CTGAGAGAGGATTTCCACCTCATCCAGTCATGTGGCCTTGGGGCATGAAGCACAC 2726
DB 2 CTGCGGGATGGCATGTCCACCTCATCCAGTCATGTGGCCTTGGGGCATGAAGCACAC 61
QY 2727 ACGGTGGTATGGGCTGGGCTTAATGCTGGCGTCAAAGCGAAGATGCCCGCGCTTGGAG 2786
DB 62 ACGGTGCTATGGCTTGGCGCGCATCTGGAAGCAGGAGACACCCCTTCTCTGGAG 121
QY 2787 ACTTTTATGGCAGTTCGAGTGACAACTGTGCGCCATCTTGCACCTGTGTGGCTAAA 2846
DB 122 AACTTGTAGACACCGTCGGCGACACACCGCGCGCACAGGCTCTGCTGGTGGCAAG 181
QY 2847 AACATCTCTCTTTCCAGCATGTGGAGCAATTTCTGAGGGCAACATTGATG 2901
DB 182 AAGCTGACGCTGTTTCCCAAAACAGGAGCGCTTCGCGGGGGGCCACATCGACG 236

RESULT 12
US-09-268-866-1
; Sequence 1, Application US/09268866
; Patent No. 6316272
; GENERAL INFORMATION:
; APPLICANT: Mack, David

; APPLICANT: Gish, Kurt C.
; APPLICANT: Wilson, Keith E.
; TITLE OF INVENTION: No. 6316272el Methods of Diagnosing of Colorectal Cancer,
; TITLE OF INVENTION: Compositions, and Methods of Screening for Colorectal
; TITLE OF INVENTION: Cancer Modulators
; FILE REFERENCE: A67474/RMS/DAV/JJD
; CURRENT APPLICATION NUMBER: US/09/268,866
; CURRENT FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4098
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-268-866-1

Query Match 2.2%; Score 92.6; DB 4; Length 4098;
Best Local Similarity 55.9%; Pred. No. 1.8e-17;
Matches 176; Conservative 0; Mismatches 139; Indels 0; Gaps 0;
QY 727 TCATGGGTGCTACCTCCCATGTCTACAAAATATTTTGGAGTGATCCTTTTACGCC 786
DB 1027 TCAAGGGTGATTAGTAGCTTGTATGTTAAACATTTGGGGTGATGCTTTTCATTAGAT 1086
QY 787 TTACATGGGTGGTGGCACAGCTGGAGTTCTTCAGGCTTTTGCATTTCTCTATCTGCT 846
DB 1087 TGTATGATTTGGTCAAGCTGGAATAGTCTATCAGTCTCTTGTATAATATGATGCCA 1146
QY 847 GCTGCTGACAAATGTGACTGCTATCTCCATGAGTGCCATTCGCACTAATGAGTGGTGC 906
DB 1147 CTGTTGTGACAACTACAGGATTTCTACTTCAGCAATAGCACTAATGAGATTGTAA 1206
QY 907 CAGCTGGGGCTCATACTTTATGATTTCCGGGCACTGGGCCAGAGTTTGTGGGGCTG 966
DB 1207 GAGGAGGAGGAGCATATTTAATATCTAGAAGTCTAGGGCCAGAAATTTGGTGTGAA 1266
QY 967 TTGGCTCTGCTTTTATCTTGTGTACCAATTTGAGAGCCATGTGACATCTTGTGTGCA 1026
DB 1267 TTGGTCTAATCTTCGCTTTGCCAAGCTGTTCAGATTGCTATGATGTGTGGATTG 1326
QY 1027 TTGAAATCTTCTGG 1041
DB 1327 CAGAAACCGTGTGG 1341

RESULT 13
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313

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/ FILING DATE:
/ APPLICATION NUMBER: EP 91 114 300.6
/ FILING DATE: 26-AUG-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BENT, Stephen A.
/ REGISTRATION NUMBER: 29,768
/ REFERENCE/DOCKET NUMBER: 30472/114 IMMU
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703)836-9300
/ TELEFAX: (703)683-4109
/ TELEX: 899149
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 7218 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ CLONE: pTZgpt-F1s
/
US-08-232-463-14

Query Match 1.4%; Score 60.6; DB 1; Length 7218;
Best Local Similarity 4.6%; Pred. No. 2.2e-07;
Matches 18; Conservative 223; Mismatches 152; Indels 0; Gaps 0;

QY 2986 TACGATCTTCACATAGCCCAATTAGAGACACACAGTATCCAAATGAGAGAGACCTAG 3045
DB |||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1437 TACRERRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1378

QY 3046 CCACCTTCTATATCACTTACGATTTAGGCGGAGTAGAGTGGTGAGATGCATGACA 3105
DB |||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1377 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1318

QY 3106 GTGATATATCAGCATATATCTACGAGCGCACCTTTGATGATGAAACAAAGGTCACGATGC 3165
DB |||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1317 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1258

QY 3166 TTCGCACATCGCGTATCCAAACAGACGACGACAGACGACCAATTTGGTGAAGACC 3225
DB |||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1257 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1198

QY 3226 GAACTCAATGCTACGATTGACACGATTTGGCTCTGATGAGACCAAGACAGACAGAACT 3285
DB |||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1197 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1138

QY 3286 ATCAGGAGAGTGCATATCTTGACAAAGACAAAGTACATGATGCATCCCGGACAAA 3345
DB |||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1137 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1078

QY 3346 AAGCAAGTCAATGAAGATTCCAGGACCTGC 3378
DB |||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1077 RRRRRRRRRRATCGAAGCTCCCTCGACCTGC 1045
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RESULT 14
US-08-232-463-14
/ Sequence 14, Application US/08232463
/ Patent No. 5670367
/ GENERAL INFORMATION:
/ APPLICANT: DORNER, F.
/ APPLICANT: SCHEIFLINGER, F.
/ APPLICANT: FALKNER, F. G.
/ TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
/ NUMBER OF SEQUENCES: 52
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley & Lardner
/ STREET: 1800 Diagonal Road, Suite 500
/ CITY: Alexandria
/ STATE: VA
/ COUNTRY: USA
/ ZIP: 22313-0299
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
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/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/232,463
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/07/935,313
/ FILING DATE:
/ APPLICATION NUMBER: EP 91 114 300.6
/ FILING DATE: 26-AUG-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BENT, Stephen A.
/ REGISTRATION NUMBER: 29,768
/ REFERENCE/DOCKET NUMBER: 30472/114 IMMU
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703)836-9300
/ TELEFAX: (703)683-4109
/ TELEX: 899149
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 7218 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ CLONE: pTZgpt-F1s
/
US-08-232-463-14

Query Match 1.2%; Score 51.8; DB 1; Length 7218;
Best Local Similarity 4.2%; Pred. No. 0.00012;
Matches 17; Conservative 222; Mismatches 165; Indels 0; Gaps 0;

QY 942 CTGGGCCACAGATTGGTGGGCTGTGGCCTCTGCTTTATCTTGTGTACCATTTGCA 1001
DB |||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1038 CTGGCTGCGAGTCGAGGAGCTTGCATTTTTTTTTTTTTTTTTTTTTTTTTT 1097

QY 1002 GCAGCCATGTACATCTTGTGTGCATTAATCTTTCTGTCTATATCGTCCCGAGCT 1061
DB |||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1098 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1157

QY 1062 GCATCTTTCACAGTATGACGACTCAAGAAATCAGACGACGATGCTAAATACATGCT 1121
DB |||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1158 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1217

QY 1122 GTCTACGCGACAGCTTCTTGGTCTTATGCTATGCTATGCTATGCTGCTAGCTAT 1181
DB |||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1218 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1277

QY 1182 GTGAACAAAGTTGCTCANTTTCTGCGCTGTGCTATGCTGCTGCTGCTGCTAT 1241
DB |||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1278 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1337

QY 1242 GCTGAGCCATCAAGTCTTCTTTGCTCTCCACACTTCCGCGTCTGATCTGGGTAA 1301
DB |||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1338 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1397

QY 1302 CGCACTCTTTCATCAACACACATGAGCTTGTGCTCTAAGACCA 1345
DB |||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1398 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYGTACCA 1441
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RESULT 15
US-09-599-360B-64
/ Sequence 64, Application US/09599360B
/ Patent No. 6548633
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Bougueleret, L.
/ APPLICANT: Jobert, S.
/ TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
/ FILE REFERENCE: GENSET.050CP3
```



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; CURRENT APPLICATION NUMBER: US/09/599,360B
; CURRENT FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/141,032
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/469,099
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent.pm
; SEQ ID NO 64
; LENGTH: 1355
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 238..1152
; NAME/KEY: sig_peptide
; LOCATION: 238..339
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: seq SIFLLSPFDSNG/KA
; NAME/KEY: polyA_signal
; LOCATION: 1298..1303
; NAME/KEY: polyA_site
; LOCATION: 1324..1355
US-09-599-360B-64

Query Match      1.0%; Score 43.2; DB 4; Length 1355;
Best Local Similarity 50.0%; Pred. No. 0.015;
Matches 108; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 4044 CATCTTACTAAGAATTTTATGTCAGTATATTGGACCTATTATCCTCGGCAAGCCAAG 4103
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1140 CATCCTGAAACTTGAAGAACTCTGGAGAAATTTCTGAAGATGTAACCAAGATCTTTCCAAA 1199
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4104 ATGCAACAATTTTATAGCTATATTTCTTTAGTATATACCCACTGCTGTAAATTTTATATTAGG 4163
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1200 TACAAGATTAGATAAATTTGCTTATTGTACTTTATGTAGAGAGAAAATTTTCAGCTTCTC 1259
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4164 ATACTTAACCTGAAACATGCGTCAGCCTCTACTCTTTCAAAAACATCCCCCAAATACC 4223
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1260 TACCCCAAGTATGAACAAGGGTGAAATTTGTGTTTAAAAATAAAACTCTTATCATGCC 1319
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4224 AGATTTAAATATCCAAAAAATAAAAAAAAAAAAAA 4259
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1320 AGCTAAAAAATAAAAAAAAAAAAAAAAAAAAAA 1355
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Search completed: November 27, 2003, 00:40:53
Job time : 232 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: November 26, 2003, 16:49:40 ; Search time 15085 Seconds
(without alignments)
11552.868 Million cell updates/sec
Title: US-09-835-976B-15
Perfect score: 4260
Sequence: 1 tsgatagaagtattcttagt.....aaaaaaaaaaaaaaaaaaaaa 4260
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2888711 seqs, 20454813386 residues
Total number of hits satisfying chosen parameters: 5777422
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

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- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sv.*
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- 15: em.ba.*
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- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
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- 37: em.htg.vrt.*
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- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	4241.4	99.6	4260	9	AF105366	AF105366 Homo sapi
2	3995.2	93.8	4453	9	AF477977	AF477977 Homo sapi
3	3657.8	85.9	3674	9	HSMB01017	AL117500 Homo sapi
4	3584.4	84.1	3767	9	AF108831	AF108831 Homo sapi
5	3445.2	80.9	3453	9	AF116242	AF116242 Homo sapi
6	2960.8	69.5	6120	10	AF211854	AF211854 Mus muscu
7	2735.2	64.2	5964	10	AF211855	AF211855 Mus muscu
8	1674	39.3	3726	6	AX401991	AX401991 Sequence
9	1674	39.3	3726	10	RNU5815	U55815 Rattus norv
10	1660.4	39.0	3734	4	OCKCC	U55053 Oryctolagus
11	1652.6	38.8	3764	10	AF121118	AF121118 Mus muscu
12	1652.6	38.8	3775	10	AF047339	AF047339 Mus muscu
13	1648.4	38.7	3613	9	AF047338	AF047338 Homo sapi
14	1648.4	38.7	3722	6	AR270566	AR270566 Sequence
15	1648.4	38.7	3722	9	HSKCC	U55054 Human K-CI
16	1646.8	38.7	3893	9	BC021193	BC021193 Homo sapi
17	1639.4	38.5	3351	4	AF028807	AF028807 Sus scro
18	1632.2	38.3	3307	4	AF515770	AF515770 Ovis arie
19	1584	37.2	3768	9	AF054506	AF054506 Homo sapi
20	1509.4	35.4	3761	9	AF054505	AF054505 Homo sapi
21	1419.4	33.3	5239	9	AF105365	AF105365 Homo sapi
22	1416.2	33.2	5155	10	AF087436	AF087436 Mus muscu
23	1395.4	32.8	3305	9	AB033002	AB033002 Homo sapi
24	1395.4	32.8	5907	9	AF208159	AF208159 Homo sapi
25	1385.2	32.5	3655	10	AF332063	AF332063 Mus muscu
26	1385.2	32.5	3656	10	AF332064	AF332064 Mus muscu
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28	1377.8	32.3	5566	10	RNU5816	U55816 Rattus norv
29	1329.4	31.2	4190	10	BC036323	BC036323 Mus muscu
30	1181	27.7	2565	9	AK026911	AK026911 Homo sapi
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35	729.2	17.1	2635	3	AK116120	AK116120 Ciona int
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38	703.4	16.5	197568	9	AC079203	AC079203 Homo sapi
39	677.8	15.9	2518	9	AK097808	AK097808 Homo sapi
40	576.6	13.5	1086	5	AF325505	AF325505 Xenopus 1
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42	514.4	12.1	2384	6	I22489	I22489 Sequence 27
43	466.8	11.0	4478	10	BC051061	BC051061 Mus muscu
44	434	10.2	489	9	F314931S01	F314931 Homo sapi
45	434	10.2	95800	9	AC021822	AC021822 Homo sapi

ALIGNMENTS

RESULT 1
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LOCUS AF105366 AF105366 4260 bp mRNA linear PRI 20-JUN-1999
DEFINITION Homo sapiens K-CI cotransporter KCC3a mRNA, alternatively spliced,
complete cds.
ACCESSION AF105366
VERSION AF105366.1 GI:5106522
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4260)
AUTHORS Mount,D.B., Mercado,A., Song,L., Xu,J., George,A.L. Jr., Delpire,E.
and Gamba,G.

TITLE Cloning and characterization of KCC3 and KCC4, new members of the cation-chloride cotransporter gene family
JOURNAL J. Biol. Chem. 274 (23), 16355-16362 (1999)
MEDLINE 99278405
PUBMED 10347194
REFERENCE 2 (bases 1 to 4260)
AUTHORS Mount, D.B.
TITLE Direct Submission
JOURNAL Submitted (10-NOV-1998) Division of Nephrology, Department of Medicine, Vanderbilt University Medical Center, S-3223 Medical Center North, Nashville, TN 37232-2372, USA

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BASE COUNT 1165 a 977 c 972 g 1146 t

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RESULT 2
AF477977 AF477977 4453 bp mRNA linear PRI 05-MAR-2002
LOCUS AF477977
DEFINITION Homo sapiens K-Cl cotransporter KCC3 variant isoform mRNA, complete cds.
ACCESSION AF477977
VERSION AF477977.1 GI:19110890
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 4453)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLES Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL Guo,J.H. and Yu,L.
Submitted (27-JAN-2002) School of Life Sciences, Institute of
Genetics, Fudan University, Handan Road, 220, Shanghai 200433,
China
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source Location/Qualifiers
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Matches 4009; Conservative 0; Mismatches 6; Indels 2; Gaps 1;
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Db 1817 TTCTGGTGGGAATCTTCTTCCCTCTGTTACAGGTATCATGCTGGAATCAACACAGATCTG 1876
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Query Match		85.9%;	Score 3657.8;	DB 9;	Length 3674;
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				Gaps	1;
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Qy	633	ACTAATCTGACTCAAGGAGCAAGGAAACATGAAGAGGCGAGAAAAATCACTGAAGGGAAA	692		
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Qy	693	AAGAAGCCCAACAGACCCCAATAGGTGACTTTCATGGGTGTCTACCTCCCATGTCTTA	752		
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Qy	933	TCCCGGCACTGGGCGCAGAGTTTGGTGGGGCTGTGGGCTCTGCTTTTATCTTGGTACC	992		
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Qy	1773	CTTTTGGTGCATGTATTGAAGGGGTGTTCTCAGAGACAAAGTTCCGTTGATGCTGTGAAA	1832
Db	1201	CTTTTGGTGCATGTATTGAAGGGGTGTTCTCAGAGACAAAGTTCCGTTGATGCTGTGAAA	1260
Qy	1833	GGAATTTGGTGTAGGCACTTATCTTGGCCATCCCATGGGTGATTTGTTATTTGGCTCC	1892
Db	1261	GGAATTTGGTGTAGGCACTTATCTTGGCCATCCCATGGGTGATTTGTTATTTGGCTCC	1320
Qy	1893	TTCTTTTCAACATGTGGGCTGGACTTTCAGAGCCTTCAAGGTGCAACGAGGCTGTACAA	1952
Db	1321	TTCTTTTCAACATGTGGGCTGGACTTTCAGAGCCTTCAAGGTGCAACGAGGCTGTACAA	1380
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LOCUS 3767 bp mRNA linear PRI 16-APR-1999
DEFINITION Homo sapiens K:Cl cotransporter 3 mRNA, complete cds.
ACCESSION AF108831
VERSION AF108831.1 GI:4585228

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Hiki,K., D'Andrea,R.J., Furze,J., Crawford,J., Woollatt,E.,
Sutherland,G.R., Vadas,M.A. and Gamble,J.R.
Cloning, characterization, and chromosomal location of a novel
human K+-Cl- cotransporter
J. Biol. Chem. 274 (15), 10661-10667 (1999)

JOURNAL
MEDLINE 99214639
PUBMED 10187864
REFERENCE
2 (bases 1 to 3767)
Hiki,K., D'Andrea,R.J., Sutherland,G.R., Vadas,M.A. and Gamble,J.
Direct Submission
TITLE
Submitted (23-NOV-1998) Human Immunology, Hanson Centre for Cancer
Research, Frome Road, Adelaide, South Australia 5000, Australia

FEATURES
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BASE COUNT 1025 a 866 c 883 g 993 t

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RESULT 5

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ACCESSION AF116242
VERSION AF116242.1 GI:6693797
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3453)

Race, J.E., Makhoul, F.N., Logue, P.J., Wilson, F.H., Dunham, P.B. and

Holtzman, E.J.

Molecular cloning and functional characterization of KCC3, a new

K-Cl cotransporter

Am. J. Physiol. 277 (6 Pt 1), C1210-C1219 (1999)

JOURNAL

MEDLINE

PUBMED

2 (bases 1 to 3453)

Race, J.E., Makhoul, F.N., Wilson, F.H., Logue, P.J., Dunham, P.B. and

Holtzman, E.J.

Direct Submission

TITLE

JOURNAL	Submitted (22-DEC-1998) Medicine, SUNY HSC, 750 E Adams St., Syracuse, NY 13210, USA
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RESULT 6

AF211854
LOCUS AF211854 6120 bp mRNA linear ROD 31-JUL-2001
DEFINITION Mus musculus K-Cl cotransporter 3a mRNA, complete cds,
alternatively spliced.
ACCESSION AF211854
VERSION AF211854.1 GI:15042076
KEYWORDS Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 6120)
AUTHORS Pearson, M.M., Lu, J., Mount, D.B. and Delpire, E.
TITLE Localization of the K(+) - Cl(-) cotransporter, KCC3, in the central
and peripheral nervous systems: expression in the choroid plexus,

JOURNAL MEDLINE PUBLISHED 21143254
REFERENCE 11246162
AUTHORS Mount, D.B., Song, L.S. and Delpire, E.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-1999) Nephrology, Vanderbilt University Medical Center, S-3223 Medical Center North, VUMC, Nashville, TN 37232, USA
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TIYS"

source

CDS

large neurons and white matter tracts
Neuroscience 103 (2), 481-491 (2001)
21143254
11246162
2 (bases 1 to 6120)
Mount, D.B., Song, L.S. and Delpire, E.
Direct Submission
Submitted (03-DEC-1999) Nephrology, Vanderbilt University Medical Center, S-3223 Medical Center North, VUMC, Nashville, TN 37232, USA
Location/Qualifiers
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RESULT 7

AF211855
 LOCUS Mus musculus k-CI cotransporter 3b mRNA linear ROD 31-JUL-2001
 DEFINITION Mus musculus k-CI cotransporter 3b mRNA, complete cds.
 ACCESSION AF211855
 VERSION AF211855.1 GI:15042078
 KEYWORDS
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 5964)
 Pearson, M.M., Lu, J., Mount, D.B. and Delpire, E.
 Localization of the K(+) -Cl(-) cotransporter, KCC3, in the central and peripheral nervous systems: expression in the choroid plexus, large neurons and white matter tracts
 Neuroscience 103 (2), 481-491 (2001)
 21143254
 11246162
 2 (bases 1 to 5964)
 Mount, D.B., Song, L.S. and Delpire, E.
 Direct Submission
 Submitted (03-DEC-1999) Nephrology, Vanderbilt University Medical Center, S-3223 Medical Center North, VUMC, Nashville, TN 37232, USA
 Location/Qualifiers
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JOURNAL	J. Biol. Chem. 271 (27), 16245-16252 (1996)
MEDLINE	96279171
PUBMED	8663311
REFERENCE	2 (bases 1 to 3726)
AUTHORS	Gillen,C.M., Brill,S., Payne,J.A. and Forbush,B. III.
TITLE	Molecular cloning and functional expression of the K-Cl cotransporter from rabbit, rat, and human. A new member of the cation-chloride cotransporter family
JOURNAL	J. Biol. Chem. 271 (27), 16237-16244 (1996)
MEDLINE	96279170
PUBMED	8663127
REFERENCE	3 (bases 1 to 3726)
AUTHORS	Payne,J.A.
TITLE	Direct Submission
JOURNAL	Submitted (18-APR-1996) John A. Payne, Human Physiology, University of California, School of Medicine, Med. Sci. Bldg. #4138, Davis, CA 95616. USA

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AUTHORS     Gillen, C.M.
TITLE       Direct Submission
JOURNAL     Submitted (15-APR-1996) Christopher M. Gillen, Cellular and
Molecular Physiology, Yale University School of Medicine, 333 Cedar
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 3764)
AUTHORS Su, W., Shmukler, B.E., Chernova, M.N., Stuart-Tilley, A.K., de Franceschi, L., Brugnara, C. and Alper, S.L.

TITLE

Mouse K-Ci cotransporter KCC1: cloning, mapping, pathological expression, and functional regulation

JOURNAL

Am. J. Physiol. 277 (5 Pt 1), C899-C912 (1999)

MEDLINE

20035026
PUBMED 10564083

REFERENCE

2 (bases 1 to 3764)
AUTHORS Shmukler, B.E. and Alper, S.L.
Direct Submission
Submitted (15-JAN-1999) Molecular Medicine Unit, Beth Israel
Deaconess Medical Center, 330 Brookline Ave., RW-663, Boston, MA
02215, USA

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QY 1790 TGAAGGGTGTCTCTCAGAGACAAAGTTCGGTGTATGCTGTGAAAGGTAAATTTGGTGGTAGG 1849
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2330 TGAGAAAGAAATGGGTGATGTTATCCGTGGGTGTCCTCTCACTGAGCCCGGTTTGTCTTT 2389
2038 CGAGAAAGAGTGGGGCGATGGGATCCGAGCCCTGTCCTGAGTGGGGCACGCTATGCACT 2097
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2510 GCTCAAAGCAGAAAGGTTTCACTATTGTTGGCTCTGTCTGATGTTGGGAACTTCTCTAGA 2569
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3298 CCGGAAGTCTACCATCTATTCCTGAGCCCCCGATGGAGTCTTTGTG 3344

RESULT 12
AF047339
LOCUS Mus musculus erythroid K:Cl cotransporter (Kcc1) mRNA linear ROD 26-AUG-1998
DEFINITION cds.
ACCESSION AF047339
VERSION AF047339.1 GI:3452286
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 3775)
AUTHORS Pellegriño, C.M., Rybicki, A.C., Musto, S., Nagel, R.L. and Schwartz, R.S.
TITLE Molecular identification and expression of erythroid K:Cl cotransporter in human and mouse erythroleukemic cells
JOURNAL Blood Cells Mol. Dis. 24 (1), 31-40 (1998)
MEDLINE 98184935
PUBMED 9516379
REFERENCE 2 (bases 1 to 3775)
AUTHORS Pellegriño, C.M., Rybicki, A.C., Musto, S., Nagel, R.L. and Schwartz, R.S.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1998) Medicine-Hematology, Montefiore Medical Center, 111 East 210th Street, Bronx, NY 10467, USA
REFERENCE 3 (bases 1 to 3775)
AUTHORS Pellegriño, C.M., Rybicki, A.C., Musto, S., Nagel, R.L. and Schwartz, R.S.
TITLE Direct Submission
JOURNAL Submitted (25-AUG-1998) Medicine-Hematology, Montefiore Medical Center, 111 East 210th Street, Bronx, NY 10467, USA
REMARK Sequence update by submitter
COMMENT On Aug 26, 1998 this sequence version replaced gi:2921848.

Query Match	38.8%;	Score 1652.6;	DB 10;	Length 3775;
Best Local Similarity	71.0%;	Pred. No. 0;		
Matches 2205; Conservative	0;	Mismatches 896;	Indels 6;	Gaps 1;

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Qy	596	GAAGGTGTCTTCCCTCCTCAAACCGCATGGCCAATTCACATAATCTGACTCAAGGAGCAAA	655
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Qy	776	TTTTTTTACGCTTTACATGGGTGGTGGGCACAGCTGGAGTTCTTTCAGGCTTTTGCATTTGT	835
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Qy	2870	TGTGAGCAATTTTCTGAGGGCAACATTGATGTGTGTGGATTCGTGATGATGGGGGAT	2929
Db	2511	CCACGAGGCTTACCTGGATGGCCATATCGACGTGTGTGGATCTGTGCATGATGAGGCGAT	2570
Qy	2930	GCTTATGTCTACTACATCTCTACTGAAACAGCAACAAGTGTGGCGAAAGTGCAGCATACG	2989
Db	2571	GCTTATGTCTGCCCCCTTCTGTCTGGCCAGCATAAAGTTTGGAAAGATGCCCGATGCG	2630
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Qy	3050	CTTCTCTATCACTTACGCATTTGAGGCGGAGTGAAGTGGTGAGATGCATGACAGTGA	3109
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RESULT 13	
AF047338	
LOCUS	AF047338 3613 bp mRNA linear PRI 26-AUG-1998
DEFINITION	Homo sapiens erythroid K:Cl cotransporter (KCC1) mRNA, complete cds.
ACCESSION	AF047338
VERSION	AF047338.1 GI:2921846
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 3613) Pellegrino,C.M., Rybicki,A.C., Musto,S., Nagel,R.L. and Schwartz,R.S.
TITLE	Molecular identification and expression of erythroid K:Cl cotransporter in human and mouse erythroleukemic cells
JOURNAL	Blood Cells Mol. Dis. 24 (1), 31-40 (1998)
MEDLINE	98184935
PUBMED	9516379
AUTHORS	2 (bases 1 to 3613) Pellegrino,C.M., Rybicki,A.C., Musto,S., Nagel,R.L. and Schwartz,R.S.
TITLE	Direct Submission
JOURNAL	Submitted (09-FEB-1998) Medicine-Hematology, Montefiore Medical Center, 111 East 210th Street, Bronx, NY 10467, USA
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Homo sapiens K:Cl cotransporter encoded by GenBank

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Best Local Similarity 71.1%; Pred. No. 0;
Matches 2196; Conservative 0; Mismatches 888; Indels 6; Gaps 1;

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DB 171 AGGAATTGACTACTATGACAGAACTGGCACTGTTTGAGGAGAGCTGGACATCCGCCC 230

QY 596 GAAGGTGTCCTCCCTCAACCGCATGGCCAAATTTACACTAATCTGACTCAAGAGCAAA 655
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QY 656 GAAACATGAAGAGGAGGAGAAACATCACTGAAGGAAAGAAAGCCACCAAGACCCCA 715
DB 291 AGAGCATGAGGAGGCGAGAGTGGGAGGAGCCCGCGGAGGCGAGCGAGGACCCAG 350

QY 716 AATGGGTACCTTCATGGGTGCTACCTCCCATGTCTACAAATATTTTGGAGTGAATCCT 775
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QY 956 TGGTGGGCTGTTGGGCTCTGCTTTATCTTGTGTACCAATTTGAGCAGGACCATGTACAT 1015
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RESULT 15
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DEFINITION Human K-Cl cotransporter (hKCC1) mRNA, complete cds.
ACCESSION U55054
VERSION 1
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REFERENCE 1 (bases 1 to 3722)
AUTHORS Gillen,C.M., Brill,S., Payne,J.A. and Forbush,B. III.
TITLE Molecular cloning and functional expression of the K-Cl cotransporter from rabbit, rat, and human. A new member of the cation-chloride cotransporter family
JOURNAL J. Biol. Chem. 271 (27), 16237-16244 (1996)
MEDLINE 96279170
PUBMED 8663127
REFERENCE 2 (bases 1 to 3722)
AUTHORS Gillen,C.M.
TITLE Direct Submission
JOURNAL Submitted (15-APR-1996) Christopher M. Gillen, Cellular and Molecular Physiology, Yale University School of Medicine, 333 Cedar St., New Haven, CT 06520, USA
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GenCore version 5.1.6
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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4048	95.0	5437	11 BC051709	BC051709 Homo sapi
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c 4	726	17.0	738	13 BU623116	BU623116 UI-H-FL1-

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ALIGNMENTS

RESULT 1
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VERSION BC033894.1 GI:21707904
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ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 4584)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapsb-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology

http://www.systemsbio.org
contact: amadan@systemsbio.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 47 Row: O Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein
This clone has the following problem: frame shifted.

FEATURES

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BASE COUNT 1209 a 1124 c 1076 g 1175 t

Query Match 96.9%; Score 4129.8; DB 11; Length 4584;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 4153; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

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DB 487 AAAAAAGCAAAATGATCTCCAGAAACACCAACCAAGATGGCTTCAGTTCGGTTCATG 546
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QY 393 CCACCCAGTGACCGGACTTCTCACCCCGCAGGATGTCATCGAGGACCTGAGTCAGAACTCC 452
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QY	4113	TTTTTTAGCTATATTTCTTTAGTATATCCCACTGCTGTAATTTTATATAGGACTACTA	4172
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QY	4173	TGAACATGGCTGAGCGCTCTACTTCTTCAAAAACATCCCCCAAAATACAGATTTAAA	4232
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QY	4233	TATCCAAAAAATAAAAAA 4252	
Db	4565	TATCCAAAAAATAAAAAA 4584	
RESULT 2			
LOCUS	BC051709	5437 bp mRNA linear HTC 14-MAY-2003	
DEFINITION		Human sapiens mRNA similar to solute carrier family 12 (potassium/chloride transporters), member 6 (CDNA clone IMAGE:5298663).	
ACCESSION	BC051709		
VERSION	BC051709.1	GI:30704980	
KEYWORDS		HTC	
SOURCE		Human sapiens (human)	
ORGANISM		Human sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS		1 (bases 1 to 5437) Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heieh, F., Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scapleton, M., Soares, M.B., Bonaldon, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Viall, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butler, M.J., Krzywicki, M.I., Skalska, U., Smal, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.	
TITLE		Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
MEDLINE		22388257	
PUBMED		12477932	
REFERENCE		2 (bases 1 to 5437)	
AUTHORS		Strausberg, R.	
TITLE		Direct Submission	
JOURNAL		Submitted (01-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
REMARK		NIH-MGC Project URL: http://mgc.nci.nih.gov	
COMMENT		Contact: MGC help desk Email: cgapb-remail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu	

Db 1936 GTACCTTCAATGGGTCTACCTCCCAAGTCTCAAAAATATTTTGGAGTGATCCCTTTT 1995
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RESULT 3
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DEFINITION BC051744 4469 bp mRNA linear HTC 14-MAY-2003
errors:
ACCESSION BC051744
VERSION BC051744.1 GI:30704365
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
MAMMALIA; EUCHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
REFERENCE 1 (bases 1 to 4469)
AUTHORS Strausberg,R.L., Feingold,B.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schnee,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,K.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,R.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalob,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettner,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallos,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
JOURNAL MEDLINE
PUBMED 12477932
REFERENCE 2 (bases 1 to 4469)
AUTHORS Strausberg,R.
DIRECT SUBMISSION
TITLE Submitted (01-MAY-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center., Stanford University School of Medicine, Stanford, CA 94305
```


Web site: <http://www.shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the J.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRK Plate: 90 Row: 1 Column: 19
 This clone has the following problem: frame shifted.

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 Matches 4003; Conservative 0; Mismatches 5; Indels 33; Gaps 3;

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 DB 430 GTTGTGACACACCGAGTCGGACCTCAGCTCTCGATCTAGTTCCCGAGTAAGATTAGCT 489
 QY 304 CCGGGGAAGCGTGGCTGAAACAAGCCGGAGTGAGCCTATGATGATGATGTCGGGGCA 363
 DB 490 CCGGGGAAGCGTGGCTGAAACAAGCCGGAGTGAGCCTATGATGATGATGTCGGGGCA 549
 QY 364 CCACTTCGCTGCAACTGTTGCACTGGATCCACCCAGTGACCGGACTTCTCACCCCCCAGG 423
 DB 550 CCACTTCGCTGCAACTGTTGCACTGGATCCACCCAGTGACCGGACTTCTCACCCCCCAGG 609
 QY 424 ATGTTCATCGAGGACCTGAGTCAGAACTCCATCACAGGGGAAACACAGCCAACTGTTAGAGC 483
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RESULT 4

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 LOCUS UI-H-FU1-bgd-h-17-0-UI-s1 NCI CGAP FU1 Homo sapiens cDNA clone
 DEFINITION UI-H-FU1-bgd-h-17-0-UI 3', mRNA sequence.

ACCESSION BU623116
 VERSION BU623116.1 GI:23289331
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 738)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished
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 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

Location/Qualifiers
 1..738
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FU1-bgd-h-17-0-UI"
 /tissue_type="Cell lines"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP_FU1"
 /note="Organ: Chondrosarcoma; Vector: pT73-Pac (Pharmacia
) with a modified polylinker; Site 1: EcoR I; Site 2: Not
 I; NCI CGAP FU1 is a normalized cDNA library derived from
 a pool of mRNA obtained from 4 cell lines from grade III
 chondrosarcoma tissues. The library was constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pT73-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is GAGGTCGGTG. The cell
 lines were provided by Dr. James Martin from the
 University of Iowa.
 TAG_LIB=UI-H-FU1
 TAG_TISSUE=Human Chondrosarcoma Grade 3 cell line mix
 TAG_SEQ=GAGGTCGGTG"

BASE COUNT 196 a 131 c 157 g 253 t 1 others
 ORIGIN

Query Match 17.0%; Score 726; DB 13; Length 738;
 Best Local Similarity 99.7%; Pred. No. 2.4e-101;
 Matches 737; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 3517 ATGAACACTACATGAGTTCTTAGAGTGCTTACCGGGGACTAGAGCGACTCTACTTG 3576
 Db 738 ATGAACACTACATGAGTTCTTAGAGTGCTTACCGGGGACTAGAGCGACTCTACTTG 679

QY 3577 TCCGGGTGGTGGCAGTGAGTATCACCATTATTTATTAACCTACTCTGAATGACCGTG 3636
 Db 678 TCCGGGTGGTGGCAGTGAGTATCACCATTATTTATTAACCTACTCTGAATGACCGTG 619
 QY 3637 CTTGACCTGTTTTCTTAAAGGCCCTACGCTCTCCAGAGTGCAGCTCATTACTACCA 3696
 Db 618 CTTGACCTGTTTTCTTAAAGGCCCTACGCTCTCCAGAGTGCAGCTCATTACTACCA 559
 QY 3697 CTCCCACTCAACTAGAGCCCTGTGTTCTGTACACATCATATCTGAATCTTGTATGAGCTGA 3756
 Db 558 CTCCCACTCAACTAGAGCCCTGTGTTCTGTACACATCATATCTGAATCTTGTATGAGCTGA 499
 QY 3757 GCCTCAAGTACCTGTGTAAAGAGCTCCCATCTCTGATCTGCAGTATTACAGAAAAAGCAA 3816
 Db 498 GCCTCAAGTACCTGTGTAAAGAGCTCCCATCTCTGATCTGCAGTATTACAGAAAAAGCAA 439
 QY 3817 ATATTTCCCTCAACATCAGAACAAATGCTCAAGCTTTTCAAGCCACTGTCTGAGCAGTCAAA 3876
 Db 438 ATATTTCCCTCAACATCAGAACAAATGCTCAAGCTTTTCAAGCCACTGTCTGAGCAGTCAAA 380
 QY 3877 GGCAAATTTAGAAATTAACAAGCTGAGCCAAATAAATGAATTTGTTAAAGGGATGCTAGAAAT 3936
 Db 379 GGCAAATTTAGAAATTAACAAGCTGAGCCAAATAAATGAATTTGTTAAAGGGATGCTAGAAAT 320
 QY 3937 TCAACTGAAGAAAAAGCAAGTCAAGTACGTATTTCAGCATTAAAGATGAATCTCAGAAG 3996
 Db 319 TCAACTGAAGAAAAAGCAAGTCAAGTACGTATTTCAGCATTAAAGATGAATCTCAGAAG 260
 QY 3997 TCATGGTTCAATGTTGACCTGTCAGGATACACTAGACAGCTTCATCTTACTTAAG 4056
 Db 259 TCATGGTTCAATGTTGACCTGTCAGGATACACTAGACAGCTTCATCTTACTTAAG 200
 QY 4057 AATTTATGGTCAAGTATATTTGGACCTATTATCTCGCAAGCCAAAGATGCAAAACATTTT 4116
 Db 199 AATTTATGGTCAAGTATATTTGGACCTATTATCTCGCAAGCCAAAGATGCAAAACATTTT 140
 QY 4117 TTAGCTATATTTCTTTAGTATACCCACTGCTGTAAATTTTATATTAGGATACTAATCGAA 4176
 Db 139 TTAGCTATATTTCTTTAGTATACCCACTGCTGTAAATTTTATATTAGGATACTAATCGAA 80
 QY 4177 ACATGGCTGAGCTCTACTCTTCAAAAACATCCCCCAAAATACCAAGATTTAAATATC 4236
 Db 79 ACATGGCTGAGCTCTACTCTTCAAAAACATCCCCCAAAATACCAAGATTTAAATATC 20
 QY 4237 CAAAAAATAAAAAA 4255
 Db 19 CAAAAAATAAAAAA 1

RESULT 5

CB998883
 LOCUS AGENCOURT_13659995 NIH_MGC_187 Homo sapiens cDNA clone
 DEFINITION IMAGE:13020565 5', mRNA sequence.
 ACCESSION CB998883
 VERSION CB998883.1 GI:30293403
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 738)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
 cDNA Library Preparation: Clontech Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM18 row: 1 column: 22
High quality sequence stop: 620.

FEATURES

source

1. .738
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30320565"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: Blood vessels - aorta, basilar and artery;
Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2:
SfiI (ggccctcgcc); 5' and 3' adaptors were used in
cloning as follows: 5' adaptor sequence:
5'-CAGCGCATATGGCC-3' and 3' adaptor sequence:
5'-ATTTCAGCGCGGAGCGGCCGACATG-TT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4 kb
(range 0.5-4.0 kb). 14/15 colonies contained inserts by
PCR. This library was enriched for full-length clones and
was constructed by Clontech Laboratories (Palo Alto, CA).
Note: this is a NIH_MGC Library."

BASE COUNT

ORIGIN

223 a 169 c 187 g 159 t
Query Match 16.4%; Score 696.6; DB 14; Length 738;
Best Local Similarity 99.2%; Pred. No. 7.5e-97;
Matches 711; Conservative 0; Mismatches 4; Indels 2; Gaps 1;
QY 3027 CAAATGAAGAAGACCTAGCCATCTTCCTATATCACTTACGCTTACGCGGAGGTAGAA 3086
DB 3 CAAATGAAGAAGACCTAGCCATCTTCCTATATCACTTACGCGGAGGTAGAA 62
QY 3087 GTGGTGAGATGATGACAGTGTATATATCAGCATATCTTACGAGGCACTTTGATGATG 3146
DB 63 GTGGTGAGATGATGACAGTGTATATATCAGCATATCTTACGAGGCACTTTGATGATG 122
QY 3147 GAACAAAGTCCAGATGCTTGGCACATGCGCTATCCAAACAGAGGACAGAGAG 3206
DB 123 GAACAAAGTCCAGATGCTTGGCACATGCGCTATCCAAACAGAGGACAGAGAG 182
QY 3207 GCACAAATGGTGAAGACCGAACTCAATGCTACGATTGACAGCACTTGGCTCTGATGAG 3266
DB 183 GCACAAATGGTGAAGACCGAACTCAATGCTACGATTGACAGCACTTGGCTCTGATGAG 242
QY 3267 GACGAAGACAGAAACCTTACGAGAGAGGTGCATGACTTTGGACAAAGACAAAGTAC 3326
DB 243 GACGAAGACAGAAACCTTACGAGAGAGGTGCATGACTTTGGACAAAGACAAAGTAC 302
QY 3327 ATGGCATCCGGGGACAAAGCGAAGTCAATGGAAGGATTCAGGACCTGCTTAAACATG 3386
DB 303 ATGGCATCCGGGGACAAAGCGAAGTCAATGGAAGGATTCAGGACCTGCTTAAACATG 362
QY 3387 CGTCCGGACAGTCCCAATGTGAGCGGATGCATACAGCAGTGAATCAACGAGGTTATA 3446
DB 363 CGTCCGGACAGTCCCAATGTGAGCGGATGCATACAGCAGTGAATCAACGAGGTTATA 422
QY 3447 GTTAAACAGTCCCATGAAGCAAGCTGGTTTATTGAATATGCCAGGGCCACCCGAAAC 3506
DB 423 GTTAAACAGTCCCATGAAGCAAGCTGGTTTATTGAATATGCCAGGGCCACCCGAAAC 482
QY 3507 CTTGAGGGTGTGAAACATACATGGAGTTCCTAGAGGTGCTTACCCAGGACCTAGAGCGA 3566
DB 483 CTTGAGGGTGTGAAACATACATGGAGTTCCTAGAGGTGCTTACCCAGGACCTAGAGCGA 542
QY 3567 GTCCTACTTGTCCGGGTGTGGCAGTGAAGTATCACCATTATTTATTCATAACCTACTCTG 3626
DB 543 GTCCTACTTGTCCGGGTGTGGCAGTGAAGTATCACCATTATTTATTCATAACCTACTCTG 602
QY 3627 AATGACCGTGTGACCTGTTTCTTAAAGGCGCTAGCTCTCCATGGAAGTGCAGCTC 3686
DB 603 AATGACCGTGTGACCTGTTTCTTAAAGGCGCTAGCTCTCCATGGAAGTGCAGCTC 662

QY 3687 ATTACTACCACTCCCACTCAACTAGAGCC--TGTTGTTCTGTACACATCATACTGAA 3741
DB 663 ATTACTACCACTCCCACTCAACTAGAGCCCTGTTGTTCTGTACACATCATACTGAA 719
RESULT 6
LOCUS BC035480 3648 bp mRNA linear HTC 31-JUL-2002
DEFINITION Homo sapiens, clone IMAGE:4943447, mRNA.
ACCESSION BC035480
VERSION BC035480.1 GI:22028104
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3648)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunnaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAP Plate: 52 Row: e Column: 9
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein
This clone has the following problem: no polyA-tail.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4943447"
/tissue_type="Brain, anaplastic oligodendroglioma with
1p/19q loss"
/clone_lib="NCI CGAP_Brn67"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
BASE COUNT 668 a 1088 c 1017 g 875 t
ORIGIN
Query Match 16.3%; Score 692.4; DB 11; Length 3648;
Best Local Similarity 61.5%; Pred. No. 1.6e-96;
Matches 1304; Conservative 0; Mismatches 562; Indels 255; Gaps 2;
QY 571 TTGAGAGAAATGACACACGACCGAGGTGTTCTTCCCTCTCAACCGCATGGCAATT 630
DB 1528 TTGATGAAGAGCTGGACATCCGCCCAAGGATTCGTCTTCTTGGGAAAGCTCGTAGCT 1587
QY 631 ACACATAATCTGACTCAAGGAGCAAGGAAACATGAAGAGGCAAGAAACATCACTGAAGGGA 690
DB 1588 ACACAACTCTACCCAGGCGCAAGAGCATGAGAGGCCGAGAGTGGGGAGGACCC 1647
QY 691 AAAAGAAGCCCAACCAAGACCCCAATGGGTACCTTTCATGGGTGTCTACCTCCCATGTC 750

Db	1648	GC	CGAGGCGAGCCGAGGACCCAGCAGATGGGCA	CCCTCATGGGGGTGTACTGCGCCTGCC	1707
Qy	751	TACAAAATATTTTTGGAGTGATCCTCTTTTTT	TACGCCCTTACATGATGGGTGGTGACACAGCTG	810	
Db	1708	TGCAGATAATCTTTGGGGTTATCCTCTCTCT	CGCGCTGACCTGGATGGTGGGACACAGCAG	1767	
Qy	811	GAGTTCCTTCAAGCCTTTTGCAATTTGTCCTT	ATCTGCTGCTGCTGTATCAATGTTGACTGTCTA	870	
Db	1768	GTGTGCTACAGGCCCTCCTCATCGTGTCTAT	TGCTGCTGTGTGTGTGTGTGTGTGTGTGTGT	1827	
Qy	871	TCTCCATGAGTGCCATTTGCCACTAATGAGT	TGGTGCCAGCTGGGGGCTCATACTTTTATGA	930	
Db	1828	TCTCCATGAGTGCCATCGCCACCAACCGT	GTGGTTCAGCTTGGGGGCTCCTATTTTATGA	1887	
Qy	931	TTTCCC	GGGCACTGGGCCCAAGAGTTTGGTGGGGCT	GTGTGGCCTCTGCTCTTTTATCTTGGTA	990
Db	1888	TCTCTCGTTCACTGGGGCCAGAAATTTGG	AGGTGCTGTGTGGCCTGTCTTCACTCGGAA	1947	
Qy	991	CCACATTTGCGAGCCATGTACATCCTTGGT	GGCCATTTGAATCTTCTGGTCTATATTCG	1050	
Db	1948	CAACATTTGCGAGCAGCCATGTACATCTG	GGGGCCATCGAGATCTTGTGACCTTACATTG	2007	
Qy	1051	TCCCCGAGCTGCCATCTTTTACAGTGAT	GACGCACCTCAAGGAATCAGCAGCCATGCTAA	1110	
Db	2008	CCCACACAGCTGCCATTTTTTACCATCG	GGTGCTCATGACAGTCCGAAATGCCACTTTGA	2067	
Qy	1111	ATAACATGCGTGTCTACGGCACAGCTTTCT	TGGTCTTATGGTATTAGTGGTATTTATCG	1170	
Db	2068	ACAATATGCGTGTATGGGACCAATTTTCT	GACCTTATGACCCCTGGTGGTGTGTGG	2127	
Qy	1171	CGGTACCGTATGTGAACAAGTTTGGCTCA	NTTTTCTGGGCTGTGTCTATTTGTCATCT	1230	
Db	2128	GGGTCAAGTATGTGAACAAATTTTGCCT	CGCTCTTTCTGGGCTGTGTGTATCATCTCCA	2187	
Qy	1231	TGGGCATCTATGCTGGAGCCATCAAGTCT	TTCTTTTGTCTCTCCACACTTCCCGTCTGCA	1290	
Db	2188	TCTCCATCTATGCTGGGGCATAAAGTCT	ATATTTGACCTTCCCGTGTTCGGGTATGCA	2247	
Qy	1291	TGCTGGGTAAACCGCACTCTTTTTCAT	CAAGACATTTGACTGATGAGTGTCTTAAGACA	CAAGGAA	1350
Db	2248	TGCTGGGCAACAGGACCCCTGCTCGCGG	ACAGATTTTGACATCTGTGCTCAAGACAGCTGTAG	2307	
Qy	1351	TTAACACATGACAGTCCCATCAAGGTTAT	GGGGATCTTCTGTACTCAGTCAATTTT	1410	
Db	2308	TGACAAATGAGACAGTGGCCACCAGAT	TGGAGTTTCTTCTGCCACAGCCCCCAACCTTA	2367	
Qy	1411	TCAATGCCACCTGTGATGAATACTTTTGT	TTCACAAATACGTCACCTTCAATCCAGGGCATTC	1470	
Db	2368	CGACCGACTCTCTGTGACCCCTACTT	CATGCTCAACAATGTGACCGAGATCCCTTGGCATCC	2427	
Qy	1471	CTGGAATGGCTAGTGGTATTAATACAG	AGAAATCTTTGGAGTAATTAACCTTACCAAGGGAG	1530	
Db	2428	CCGGGGCAGCTGCTGTGTGCTCCAGG	AAAAACCTGTGGAGCGCTACTCGGAGAGGGTG	2487	
Qy	1531	AGATC-----ATCGAAAAGCCTTCAG	CCCAATCTTCTGATGTCTTAGGCAGCTTAAACCA	1585	
Db	2488	ACATCTGGAGAGCATGGGCTGGCCCT	CCGAGATGCCCGAGGCTGAAGGAGAGCCTGCC	2547	
Qy	1586	TGAATATGTTCTTGTGACATCAACACT	CTCTTACGCTTCTGGTGGGAATCTTCTTTCC	1645	
Db	2548	TCTGTAGTGGTGCCTGACATCGCCAC	ATCTTCACGTCTGGTGGCATCTTCTTCCC	2607	
Qy	1646	CTCTGTTACAGGTATCATGGCTGGAT	CAAAACAGATCTGGAGATCTGAAGATGCTCAGAA	1705	
Db	2608	TTCTGTAAACAGGCATCATGGCTGGCT	CAAAACCGCTCTGGGGAACCTTGTGACGCCAGAA	2667	
Qy	1706	GTCTATTTCCGATGGTACTACTTCTT	GGCATCTTGAACCACTCTCTTGTGTAT-----	1757	
Db	2668	GTCTATCCCTGTGGGGACCAATCT	GTGGCCATTTACAACATCTCCCTGTGTGTATCTTTC	2727	
Qy	1758	-----	-----	1757	

Db	2728	CCAGGCCTGGGGCAGGTTGGGGCAGAGACGGGAAGCGCTTTGGCGTGTGTACGTTGGCCAGG	2782
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Db	2788	TCACATGCACAGACACCCACACACTCATATATAGCTCCCTTCTCATGCACACATGCAC	2847
Qy	1758	-----	1757
Db	2848	ATACACACACGAGACTCCAGCTGTAGGTGTCTCTGTAGTCTGTGGCTGGGTGGGGGCAC	2907
Qy	1758	-----	1757
Db	2908	GTGGTACTATTACGGGACAGTGGGGTGGCAGAGGCCGAGTTTCTTTGACGCCGCCGCAG	2967
Qy	1758	--TTAAGCAATTTGTCTCTTTTGGTGCATGTATTGAAGGGGTTGTCTCTCAGAGACAAAGT	1815
Db	2968	ACTTCAGCAGTGTGGTTCTCTTTGGTGCCTGCATTGAGGGTGTGGTTCTCCGGGACAAAGT	3027
Qy	1816	TCGGTGTATGCTGTGAAGAGTAAATTTGGTGTGTAGCACCCTTATCTTTGSGCCAATCCCATGGG	1875
Db	3028	ATGGCATGTGTGTGACGAGGAACCTGGTGGTGGGCAACCTGGGCTGGGCTTCACTCCCTGGG	3087
Qy	1876	TGATTGTATTGGCTCCCTCTCTTTTCAACATGTGGGCTGGACTTCAGAGGCTCACAGGTG	1935
Db	3088	TCATCGTCACTGGGCTCCCTCTCTTTTCAACGTGTGGGCTGGCCCTCAGAGGCTCACAGGGG	3147
Qy	1936	CACCGAGGCTGTACAAAGCTATTGCCAAGGATAAACAATACATACCGTTTCTCAGAGGTTTTCG	1995
Db	3148	CACCACGCTATTGACAGGCCATTGGCCAAAGACAACATCATCCCTCCTGACGGCACTCATCGCG	3207
Qy	1996	GCCACAGCAAGCCAAATGGGGAACCTACCTGGGCTTTTACTTTAACTGTCTGCCATTGCGAG	2055
Db	3208	GCCACGGGAAGGTGAATGGTGAACCCACATGGGCACCTCCTCCTGACGGCACTCATCGCG	3267
Qy	2056	AGCTTGAATACTCATTTGGCTCCCTGGATCTTGTGGCCCAATCTTTCCATGTTTTC	2115
Db	3268	AGCTGGGCATCTCATCGCCCTCCCTCGACATGGTGGCCCCCATCTTATCCATGTTCTTTC	3327
Qy	2116	TCATGTGTTACCTCTTTGTAAACTTGGCATGTGCCTTGCACAACTACTTCGAACACCCCA	2175
Db	3328	TGATGTCTACCTGTTCTGTAACTCGCTGTGGGTGACAGACCTCTTGAGACCCCCCA	3387
Qy	2176	ACTGGAGACCCCGATTCGGCTACTACCATTTGGGCCCTTTCTTTTCATGGGAATCAGTATCT	2235
Db	3388	ACTGGGCCCCCGTTCAAGTACTATCACTGCGCGCTGCTCTTCTGGGCATGAGTCTCT	3447
Qy	2236	GTCTGGCTCTGATGTTTCAATTTCTCTCTGGTATTATGCCATTGTAGCCATGGTAAATAGCTG	2295
Db	3448	GCCTGGGCCCTTATGTTGTCTCTCTCTGGTACTATGCCCTGGTGGGCATGCTCATCGCGC	3507
Qy	2296	GTATGATCTACAAGTACATTTGAATACCAAGGAGCTGAGAAAGAAATGGGGTGAATGGTATCC	2355
Db	3508	GCATGATCTACAATAATCATCGAGTACCAAGGGGCTGAGAAGGAGTGGGTGACGGGATCC	3567
Qy	2356	GTGGGCTGTCCCTCAGTGCAGCCCGTTTGTCTTTGCTTCGATTGGAGGAGGACCTCCAC	2415
Db	3568	GAGGCTGTCCCTGAGCGCTGCCCGCTAGCGCTGTTGGGCTGGAGGAGGGGSCCTCCTC	3627
Qy	2416	ACACTAAAACCTGAGGCGCTC	2436
Db	3628	ACACCAAGAACTGGCGCGCGC	3648
RESULT 7			
BG776289			
LOCUS			
DEFINITION			
602663357F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4808366 5',			
mRNA sequence.			
ACCESSION			
BG776289			
VERSION			
BG776289.1 GI:14046606			
KEYWORDS			
EST.			
SOURCE			
Homo sapiens (human)			
ORGANISM			
Homo sapiens			
linear			
EST 15-MAY-2001			

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLC1661 row: b column: 15
High quality sequence stop: 735.

Location/Qualifiers
1. .749

FEATURES

source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:480366"

/issue_type="mucoepidermoid carcinoma"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH MGC 59"

/note="Organ: lung; Vector: pDNR-LJB (Clontech); Site_1:
SfiI (ggcgctggcc); Site_2: SfiI (ggcattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGGCGGCGGACATG-DT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."

BASE COUNT 172 a 188 c 182 g 207 t

ORIGIN

Query Match 15.9%; Score 678; DB 12; Length 749;

Best Local Similarity 98.5%; Pred. No. 5.2e-94;

Matches 726; Conservative 0; Mismatches 6; Indels 5; Gaps 4;

1 TTCTGAGGGTTTGGCCACAGCAAGCCCAATGGGAACCTACCTGGGCTTACTTCTAA 2040

1 TTCTGAGGGTTTGGCCACAGCAAGCCCAATGGGAACCTACCTGGGCTTACTTCTAA 60

2041 CTGCTGCATTGCAGAGCTTGGAACTACTCATTCCTCCCTGGATCTTGTGGCCCAATTC 2100

61 CTGCTGCATTGCAGAGCTTGGAACTACTCATTCCTCCCTGGATCTTGTGGCCCAATTC 120

2101 TTTCCATGTTTTTCTCANGTGTACCTCTTTCTAAACTTGGCATGTGCTTGCACAAAT 2160

121 TTTCCATGTTTTTCTCANGTGTACCTCTTTCTAAACTTGGCATGTGCTTGCACAAAT 180

2161 TACTTGAAACCAACCACTGAGACCCCGATTCGCTACTACCACTGGGCCCTTCTTCA 2220

181 TACTTGAAACCAACCACTGAGACCCCGATTCGCTACTACCACTGGGCCCTTCTTCA 240

2221 TGGGAATGAGTATCTGTCTGGCTCTGATGTTTCTTCTTCTGTTATGTCATTTAG 2280

241 TGGGAATGAGTATCTGTCTGGCTCTGATGTTTCTTCTTCTGTTATGTCATTTAG 300

2281 CCATGGTAATAGCTGGTATGATCTACAAGTACATTTGAATACCAAGAGCTGAGAAAGAT 2340

301 CCATGGTAATAGCTGGTATGATCTACAAGTACATTTGAATACCAAGAGCTGAGAAAGAT 360

2341 GGGGTGATGATATCCGTTGGGCTGCTCCTCAGTCAGCCCGGTTGCTTTCGATTGG 2400

361 GGGGTGATGATATCCGTTGGGCTGCTCCTCAGTCAGCCCGGTTGCTTTCGATTGG 420

QY 2401 AGGAAGACCTCCACACACTAAAACTGGAGGCTCAGTTGC-TTGTTATTACTGAAACTA 2459

Db 421 AGGAAGACCTCCACACACTAAAACTGGAGGCTCAGTTGC-TTGTTATTACTGAAACTA 480

QY 2460 GATGAAGACTTACATGTCAAGCATCCTCGCTCTCCTCAGCTTGTGCTCAGCTCAAGCA 2519

Db 481 GATGAAGACTTACATGTCAAGCATCCTCGCTCTCCTCAGCTTGTGCTCAGCTCAAGCA 540

QY 2520 -GGAAAAAGTNTCACTATTGTGGGCTCTGTCTCATCGTGGGAACTTCTCTAGAGAACTACGG 2578

Db 541 CGGAAGAGTCTCACTATTGTGGGCTCTGTCTCATCGTGGGAACTTCTCTAGAGAACTACGG 600

QY 2579 TGAAGCTTTAGCTCTCAGCAGACCATAAAGACCTAATGAGGAGAGAGGT--AAAA 2636

Db 601 TGAAGCTTTAGCTCTCAGCAGACCATAAAGACCTAATGAGGAGAGAGGT--AAAA 660

QY 2637 GGATTCGCCAGCT-GGTGGTGGCGGCGCAAGCTGAGAGAGGGCATTTCCACCTCATCCA 2695

Db 661 GGATTCGCCAGCTGGGTGGTGGCGGCGCAAGCTGAGAGAGGGCATTTCCACCTCATCCA 720

QY 2696 GTCATGTGGCTTGGGG 2712

Db 721 GTCATGTGGCTTGGGG 737

RESULT 8

BM702804

LOCUS

DEFINITION

UI-E-CK1-afh-e-15-0-UI.r1 UI-E-CK1 Homo sapiens cDNA clone

UI-E-CK1-afh-e-15-0-UI 5', mRNA sequence.

ACCESSION

BM702804

VERSION

BM702804.1 GI:19016062

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 666)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalizaton and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).

Seq primer: M13 Reverse.

Location/Qualifiers

1. .666

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-E-CK1-afh-e-15-0-UI"

/tissue_type="Retina Foveal and Macular"

/dev_stages="adult"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone_lib="UI-E-CK1"

/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a

modified polylinker; Site 1: EcoR I; Site 2: Not I;

UI-E-CK1 is a normalized cDNA library containing the

following tissue(s): Retina Foveal and Macular. The

library was constructed according to Bonaldo, Lennon and

Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dr)18 tail. The sequence tag for this library is GTCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT 215 a 144 c 137 g 170 t

ORIGIN

Query Match 15.4%; Score 655; DB 12; Length 666;
Best Local Similarity 99.9%; Pred. No. 1.8e-90;
Matches 666; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 3427 TGAACCTCAACGAGGTATAGTTAAACAGTCCCATGACCAAGCTGGTTTATTGAATA 3486
Db |||||
1 TGAACCTCAACGAGGTATAGTTAAACAGTCCCATGACCAAGCTGGTTTATTGAATA 60
QY 3487 TGCCAGGGCCACCCGAAACCTCGAGGTCATGAAACCTACATGAGTTCCTAGAGGTGC 3546
Db |||||
61 TGCCAGGGCCACCCGAAACCTCGAGGTCATGAAACCTACATGAGTTCCTAGAGGTGC 120
QY 3547 TTACCGAGGACTAGAGCGAGTCTTACTTGTCCGGGTGGTGGCAGTGAAGTATCACCA 3606
Db |||||
121 TTACCGAGGACTAGAGCGAGTCTTACTTGTCCGGGTGGTGGCAGTGAAGTATCACCA 180
QY 3607 TTTATTTCATACCTACTCTGAATGACCGTGTGACCTGTTTCTTAAAGCCCTACGTC 3666
Db |||||
181 TTTATTTCATACCTACTCTGAATGACCGTGTGACCTGTTTCTTAAAGCCCTACGTC 240
QY 3667 TCCCATGGAAGTCCAGCTCTTACTTACCCTCCCACTCAACTAGAGCTGCTGTTCTGT 3726
Db |||||
241 TCCCATGGAAGTCCAGCTCTTACTTACCCTCCCACTCAACTAGAGCTGCTGTTCTGT 300
QY 3727 ACACATCATCTAACTCTTGATGAGCTGAGCTCAAGTACCTGTGTAAAGAGCTCCCA 3786
Db |||||
301 ACACATCATCTAACTCTTGATGAGCTGAGCTCAAGTACCTGTGTAAAGAGCTCCCA 360
QY 3787 TCTGATCTGCAGTCACTACAGAAAAGCAAAATATTCCTCAACATCAGAACAACTCTCA 3846
Db |||||
361 TCTGATCTGCAGTCACTACAGAAAAGCAAAATATTCCTCAACATCAGAACAACTCTCA 420
QY 3847 GTCTTTCAAGCCACTGTCTGACAGTCAAGGCAAAATAGAAATTAACAGCTGAGCCAAT 3906
Db |||||
421 GTCTTTCAAGCCAC - GTCTGACAGTCAAGGCAAAATAGAAATTAACAGCTGAGCCAAT 479
QY 3907 AAATGAATTGGTAAAGGATGCTAGAAAATTCAACTGAAGAAAAAAGCAAGTCAAGTAC 3966
Db |||||
480 AAATGAATTGGTAAAGGATGCTAGAAAATTCAACTGAAGAAAAAAGCAAGTCAAGTAC 539
QY 3967 GTATTTCAGCATTAAGATGAATCTCAGAGTCAATGTTCAATGTTGACACTGTGAGGATA 4026
Db |||||
540 GTATTTCAGCATTAAGATGAATCTCAGAGTCAATGTTCAATGTTGACACTGTGAGGATA 599
QY 4027 ACAACTAGAGACAGCTTCACTTCTTAAAGAAATTTATGCTCAAGTATATTTGGACCTATT 4086
Db |||||
600 ACAACTAGAGACAGCTTCACTTCTTAAAGAAATTTATGCTCAAGTATATTTGGACCTATT 659
QY 4087 ATCTCTCG 4093
Db |||||
660 ATCTCTCG 666

RESULT 9
BI731141
LOCUS 603351795F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5359319 5',
DEFINITION mRNA sequence.
ACCESSION BI731141

BI731141.1 GI:15708154
EST.
Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 778)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11913 row: n column: 24
High quality sequence stop: 770.
Location/Qualifiers
1..778
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:5359319"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
BASE COUNT 174 a 197 c 204 g 203 t
ORIGIN

Query Match 14.9%; Score 636.8; DB 12; Length 778;
Best Local Similarity 89.8%; Pred. No. 1e-87;
Matches 694; Conservative 0; Mismatches 78; Indels 1; Gaps 1;

QY 2091 GCCCAATCTCTTCATGTTTTTTTCTCATGTGTACCTCTTTGTAACCTGGCATGTGCC 2150
Db |||||
6 GCCCAATCTCTTCATGTTTTTTTCTCATGTGTGTGCGCTCTTTGTGAACCTGGCTTGTGCC 65
QY 2151 TTGCAAACTTACTTCGAACACCAACCTGGAGACCCGATCCCGTACTACCATTTGGGCC 2210
Db |||||
66 TTGCAAACTTGTGCGAACCCCAACCTGGAGGCTCGATTCGCTATATACATCGGGCC 125
QY 2211 CTTTCTTTTCATGGGAATGAGTATCTGTCTGCTCTGTATGTTTCATTTCTTCTGGTATTAT 2270
Db |||||
126 CTCTCTTTTCATGGGAATGAGTATCTGTCTAGCTCTGTATGTTTCATTTCTTTGGTATTAT 185
QY 2271 GCCATTTAGCCATGGTAATAGCTGGTATGATCTACAAGTACATTTGAATACCAAGGAGCT 2330
Db |||||
186 GCCA - TGTAAGTATGTAATAGCTGGCATGATCTACAAGTACATTTGAATACCAAGGAGCT 244
QY 2331 GAGAAAGTGGGGTGTGATCCGTGGGCTGTCCTCAGTCGAGCCCGGTTGCTTTG 2390
Db |||||
245 GAGAAAGTGGGGGATGGTATCCGTGGGCTGTGCTCAGTCGAGCCCGCTTGCCTTTG 304
QY 2391 CTTGATTTGGAGGAGGACCTCCACACACTAAAACTGGAGGCTCAGTGTCTGTATTATTA 2450
Db |||||
305 CTCTGCTTAGAGGAGGACCTCTCCACACTAAAACTGGAGGCTCAGTGTCTGTCTCTA 364
QY 2451 CTGAAACTAGATGAAGACTTACATGTCAAGCATCTCGCTCTCCACCTTTGCTTCACAG 2510
Db |||||
365 CTGAAGCTGGATGAAGATTTACAGCTCAAGCACCTCGCTCTCCACCTTTGCTTCACAG 424
QY 2511 CTCAAGCAGGAAAGGTTTACATTTGTGGGCTCTGTATCGTGGGGAACCTTCTCTAGAG 2570
Db |||||
425 CTCAAGCAGGAAAGGACTCAACGATTTGTGGGCTCTGTATCGTGGGGAACCTTCTCTAGAG 484

QY 2571 AACTACGGTGAAGCTTTAGCTGCTGAGCAGACCATAAACACCTAATGTGAGGAGAGAG 2630
 |||||
 Db 485 AACTATGGTGACGGCTCGCGGAGAGAGACCAATTAGCACTAATGGAGGAGAGAG 544
 |||||
 QY 2631 GTAAAGAGATTCTGCGAGCTGGTGGGCGGCAAGCTGAGAGAGGCAATTTCCACCTC 2690
 |||||
 Db 545 GTAAAGAGATTCTGCGAATTGGTGGTGGCTGCGCAAGCTGAAAGAGGGCATATCACACCTC 604
 |||||
 QY 2691 ATCCAGTCTGCGCTTGGGGCATGAGCAGACACACAGCTGGTGGCTGGCTGAGTG 2750
 |||||
 Db 605 ATCCAGTCTGCGCTTGGGGCATGAGCAGACACACAGCTGGTGGCTGGCTGAGTG 664
 |||||
 QY 2751 GGTGCGCTCAAGCGCAAGATGCCGCGCTTGGAGACTTTTATTGGCAGCTGGAGTG 2810
 |||||
 Db 665 GGTGCGCTCAGAGTGAAGATGCTGCGCTTGGAGACTTTTATTGGCAGCTGGAGTG 724
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 QY 2811 ACAACTGTGCCCATCTTGCACCTGCTGGTGGCTGAAACATCTCCTTTCTTCC 2863
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 Db 725 ACAACTGTGCCCATCTAGCCCTGCTGGTGGCTGAAATGCTCCTTCTTCC 777
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RESULT 10

BI825527
 LOCUS 603072276F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5164098 5',
 mRNA sequence.

ACCESSION BI825527

VERSION BI825527.1 GI:15937077

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE 1 (bases 1 to 905)

JOURNAL NIH-MGC <http://mgc.nci.nih.gov/>.

COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11407 row: h column: 19

High quality sequence start: 9

High quality sequence stop: 746.

Location/Qualifiers

1. .905

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5164098"

/tissue_type="medulla"

/lab_host="DH108"

/clone_lib="NIH_MGC_119"

/notes="Organ: Brain; Vector: pCMV-SPORT6; Site: 1; NotI;

Site 2: EcoRV (destroyed); RNA source normal medulla from

anonymous male age 27. Library is oligo-dr primed and

directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.3 kb, insert size range

0.9-3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 013. Note:

this is a NIH MGC Library."

BASE COUNT 218 a 233 c 227 g 227 t

ORIGIN

Query Match 14.7%; Score 627.8; DB 12; Length 905;

Best Local Similarity 91.8%; Pred. No. 2.2e-86;

Matches 766; Conservative 0; Mismatches 48; Indels 20; Gaps 9;
 QY 240 CCAGTTTGTGACAGACACAGTCCGACNTAGCTCTCGATCTAGTTCGCCAGTAAGATT 299
 |||||
 Db 71 CAAGTTTGTGACAGACACAGTCCGACCTAGCTCTCGATCTAGTTCGCCAGTAAGATT 130
 |||||
 QY 300 AGCTCCCGGGAAGCGTGCCTGA--AACAGCCGAGTGAAGCTATGAGTGAAGATCTGG 358
 |||||
 Db 131 AGCTCCCGGGAAGCGTGCCTGATAACAAGCCGAGTGAAGCTATGAGTGAAGATCTGG 190
 |||||
 QY 359 GGCACACACTTCGCTGGCAACTGTGCACTG-GATCCACCCAGTGAACCGGACTTCTCACC 417
 |||||
 Db 191 GGCACACACTTCGCTGGCAACTGTGCACTGCACTCCACCCAGTGAACCGGACTTCTCACC 250
 |||||
 QY 418 CCCAGAGTTCATCGAGGACCTGAGTCAAGAACTCCATCACAGGGGAACACAGCCAACTGT 477
 |||||
 Db 251 CCCAGAGTTCATCGAGGACCTGAGTCAAGAACTCCATCACAGGGGAACACAGCCAACTGT 310
 |||||
 QY 478 TAGACGCGGACATAAGAAAGCTCGAAATGCTTATCTCAATAATTTCCAAATTATGAAGAAG 537
 |||||
 Db 311 TAGACGCGGACATAAGAAAGCTCGAAATGCTTATCTCAATAATTTCCAAATTATGAAGAAG 370
 |||||
 QY 538 GAGATGAATATTTGATTAATAAATTTGGCACTCTTTGAGGAAGAAATGACACACACCGA 597
 |||||
 Db 371 GAGATGAATATTTGATTAATAAATTTGGCACTCTTTGAGGAAGAAATGACACACACCGA 430
 |||||
 QY 598 AGGTGTCTTCCCTCCTCAACCGCATGGCCAAATACACTAACTGACTCAAGGAGCAAAAGG 657
 |||||
 Db 431 AGGTGTCTTCCCTCCTCAACCGCATGGCCAAATACACTAACTGACTCAAGGAGCAAAAGG 490
 |||||
 QY 658 AACATGAAGAGCGCAGAAAACATCACTGAAGGGAAGAAAGACCCACCAAGACCCCAAAA 717
 |||||
 Db 491 AACATGAAGAGCGCAGAAAACATCACTGAAGGGAAGAAAGACCCACCAAGACCCCAAAA 550
 |||||
 QY 718 TGGGTACCTTCATGGGTGTCTACCTCCCATGTCTACAAAATATTTTGGAGTATCCTTT 777
 |||||
 Db 551 TGGGTACCTTCATGGGTGTCTACCTCCCATGTCTACAAAATATTTTGGAGTATCCTTT 610
 |||||
 QY 778 TTTTACGCTTTACATGGGTGTGGGCGACAGC-TGGAGTTCTTCAGGCTTTTGC-AATTGT 835
 |||||
 Db 611 TTTTACGCTTTACATGGGTGTGGGCGACAGCTTGGAGTTCTTCAGGCTTTTGC-AAATTGT 670
 |||||
 QY 836 CTTTATCTGCTGCTGTACAAATGTTGACTGTCTATCTCCATGAGTGCCATTTGCCACTAA 895
 |||||
 Db 671 CTTTATCTGCTGCTGTACAAATGTTGACTGTCTATCTCCATGAGTGCCATTTGGCACTAA 730
 |||||
 QY 896 --TGGAGTGGTCCAGCTGGGGGCTCACTACT-----TTATGATTTCCCGGGCACTGGG 946
 |||||
 Db 731 ATGGGAGTGGTCCAGCTGGGGGCTCACTACTCTAATGAATTTCCGTCGACCTGGG 790
 |||||
 QY 947 CCCAGAGTTTGG--TGGGGCTGTTGGCCTCTGCTTTTATCTTGGTACACACTTT--GCA 1001
 |||||
 Db 791 CCCAGAGTGGTGGGGCTGTTGGACCTCTGCTTTTATCTTGGTACACACTTTGGGCGAG 850
 |||||
 QY 1002 CGAGCCATGTACATCTTTGGTGCCATT--GAAATCTTTTGGTCTATATCGTCC 1053
 |||||
 Db 851 CGGGCATGTTTCATCACTGGGTGGCTTTGAAAATCTCTCTGSGTCTATATCGTCC 904
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RESULT 11

CA325003

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 723)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

CA325003 723 bp mRNA linear EST 26-NOV-2002

UI-M-FY0-cem-1-01-0-UI_r1 NIH_BMAP_FY0 Mus musculus cDNA clone

IMAGE: 6821618 5', mRNA sequence.

CA325003

CA325003.1 GI:24543101

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.
 Location/Qualifiers
 1. 723
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE: 6821618"
 /tissue_type="whole brain"
 /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH_BMAP_FY0"
 /note="Organ: Brain; Vector: pYX-Asc; Site: 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is ACCGAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

BASE COUNT 201 a 162 c 207 g 153 t

Query Match 14.5%; Score 619; DB 14; Length 723;
 Best Local Similarity 91.0%; Pred. No. 5.5e-85;
 Matches 658; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 2611 ACCTAATGGAGCAGAGAGGTAAAGGATTTCTGCCAGTGTGTGGCCGCAAGCTGA 2670
 DB 1 ACCTAATGGAGCAGAGAGGTAAAGGATTTCTGCCAGTGTGTGGCCGCAAGCTGA 60
 QY 2671 GAGAGGGCATTTCCACACCTCATCCAGTCTATGTGGCTTGGGGCCATGAAGCACACACGG 2730
 DB 61 AGAGGGCATTTCCACACCTCATCCAGTCTGTGGCTCGGAGGCATGAACACACACAG 120
 QY 2731 TGGTGATGGCTGGCTTAATGGCTGGCGTCAAGCGCAAGATGCCCGCTGGAGAGCTT 2790
 DB 121 TGGTGATGGCTGGCGCAATGGCTGGCGTCAAGTGAAGATGCTCGCGCTTGAAGAGCTT 180
 QY 2791 TTATTGGCNCAGTTGAGTGACAACCTGCTGCCCATCTTGCATGCTGGTGGCTAAACACA 2850
 DB 181 TCATTGGCNCAGTACGAGTGACAACCTGCTGCCCATCTAGCCCTGCTGGTGGCTAAACATG 240
 QY 2851 TCTCTCTCTTCCAGCAATGTGGAGCAATTTCTTGAGGGCAACATTTGATGTGTGTGA 2910
 DB 241 TCTCTCTCTTCCAGCAATGTGGAGCAGTTTCTTGAGGGCAACATTTGATGTGTGTGA 300
 QY 2911 TTGTCATGATGGGGGATGCTTATCTACTACCTACCTACTGTAAGACAGCAAGAGTGT 2970
 DB 301 TTGTGCATGATGGGGGATGCTTATCTACTACCTACTGTAAGACAGCAAGAGTGT 360
 QY 2971 GCGGAAGTGCAGCATCGGATCTTCACAGTAGGCCCAATTAGACAGCAACAGTATCCAAA 3030

Db 361 GCGGAANTGCAGCATACGGATCTTCACAGTAGCCCACTAGAAGACAAACAGTATCCAGA 420
 QY 3031 TGAAGAAGGACCTAGCCACCTTCTCTATATCTACTTACGCAATTCAGCGGAGGTAGAAGTGG 3090
 Db 421 TGAAGAAGGATCTGGCCACCTTTCTGTACCACTTGGCGCATTCGAGCAGAAGTGAAGTGG 480
 QY 3091 TGGAGATGCATGACAGTGAATATATACAGATATATCTACGAGCGCACTTTGATGTGAAC 3150
 Db 481 TGGAGATGCACGACAGTGAATATATCTGCTATATATGAGCGCACCTCTGATGTGAGC 540
 QY 3151 AAAGTCCAGATGCTTCGGCACATGCGGCTATCCAAAACAGAGCGACAGAGAGGCAC 3210
 Db 541 AGAGTCCAGATGCTTCGGCATATGCGGCTGTCCAAAACAGAGCGACAGAGAGGCAC 600
 QY 3211 AATTGGTGAAGACCGAAACTCAATGTCTACGATTCAGCAGCATTTGGCTCTGATGAGGACG 3270
 Db 601 AGCTGGTGAAGATCGAAACTCAATGTCTACGATTCAGCAGCATTTGGCTCTGATGAGGACG 660
 QY 3271 AAGAGACAGAAACCTATCAGGAGAGGTGACATGACTTTGGACAAAACAGAAAGTACATGG 3330
 Db 661 AAGAGACAGAAACCTATCAGGAGAGGTGACATGACTTTGGACAAAACAGAAAGTACATGG 720
 QY 3331 CAT 3333
 Db 721 CAT 723

RESULT 12

CD350624 719 bp mRNA linear EST 29-MAY-2003
 UI-M-G10-cgg-m-22-0-UI.r1 NIH_BMAP_G10 Mus musculus cDNA clone
 IMAGE: 6853151 5', mRNA sequence.
 CD350624
 ACCESSION CD350624.1 GI:31142139
 VERSION EST.
 KEYWORDS Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 719)
 NIH-MGC <http://mgc.nci.nih.gov/>
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/mousefl.html>
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.

Location/Qualifiers
 1. 719
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE: 6853151"
 /tissue_type="whole brain"
 /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH_BMAP_G10"
 /note="Organ: Brain; Vector: pYX-Asc; Site: 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned

directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is ACCGAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): "Gene Discovery in the Developing Mouse Nervous System", supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

BASE COUNT 146 a 192 c 164 g 216 t 1 others

Query Match 14.0%; Score 597; DB 14; Length 719;
Best Local Similarity 89.3%; Pred. No. 1.3e-81;
Matches 642; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 743 CCCATGCTACAAATATTTTGGAGTGATCTTTTACGCCCTTACATGGTGGG 802
DB 1 CCATGCTACAGAACATCTTTGGAGTGATCTTCTCGCTTACCTGGGTAGTGG 60
QY 803 CACAGCTGGAGTCTTTCAGGCTTTTGCATTTGCTTATCTGCTGCTGTACAAATGTT 862
DB 61 AACAGCTGGAATCCTTCAGGCTTTTGCATTTGCTTATCTGCTGCTGTACAAATGTT 120
QY 863 GACTGCTATCTCATGAGTGCCATGTCCTAATAGAGTGGTGCAGCTGGGGGTCTATA 922
DB 121 AACTGCCATCTCATGAGGCCATGCCACTAACGAGTGGTGCAGCTGGGGGTCTATA 180
QY 923 CTTTATGATTTCCGGGCACTGGGCCAGAGTTTGGTGGGCTGTGGCCTGCTTTTA 982
DB 181 CTTTCATGATTTCCAGAGCCCTGGGCCAGAGTTTGGGGGGCTGTAGGCTCTGCTTTTA 240
QY 983 TCTTGTGTACCAATTTGCAGCAGCCATGTACATCTTGTGTCATTTGCAATCTTTCTGT 1042
DB 241 TCTTGCACACATTTTGCAGCAGCCATGTATCTTGTGTCATTTGCAATCTTTCTGT 300
QY 1043 CTATATCTGCCCGAGCTGCCATCTTTACAGTGAAGCAGCACTCAAGAAATCAGCAGC 1102
DB 301 ATACATTTGTCGCCGAGCTGCCATCTTTCGAGTGACGATGCACTCAAGGAGTCAGCAGC 360
QY 1103 CATGCTAAATACATCGCTGTCTACGGCAGCTTTCTTGGTCTTATGTTAGTGGT 1162
DB 361 TATGCTGAACAACATCGCGCTCTATGCTACAGCTTTCTTGGTCTCAAGGCTTGTGGT 420
QY 1163 ATTTATCGGCGTACGCTATGTGAACAAGTTTGCTCANTTTTCTGGCCTGTGTCTATTGT 1222
DB 421 ATTATCGGCGTACGCTATGTGAATAGTTTGCCTCACTCTTCTGGCCTGTGTATTGT 480
QY 1223 GTCATCTTGGCCATCTATGCTGGAGCCATCAAGTCTTTTGTGCTCCACACTTCCC 1282
DB 481 GTCGATCTTGGCTATCTATGCTGGTGCATCAAGTCTTCTTGTCTCCACCACTTCCC 540
QY 1283 GGTCTGATGCTGGGTAAACCGCACTTTTCATCAAGACACATTTGAGCTTTGCTTAAGAC 1342
DB 541 GGTCTGATGCTGGGCAACCGTACCTGTGTCATCAAGACACCTTGTGCTTAAAGAC 600
QY 1343 CAAGGAAATTAACAACATGACAGTCCCATCAAGTTATGGGATTTCTTGTAACTCCGAG 1402
DB 601 CAAGGAGTTGACAAATGACATGACATCAATCAAGTTATGGGATTTCTTGTCACTCCAG 560
QY 1403 TCAATTTTCAATGCCACCTGTGATGAATCTTTGTTCAAPACAGTCACTTCAATCC 1461
DB 661 TCAGTTCTTTAATGCCACCTGTGATGAGTACTTTGTTTCAANNTAGCTATCTCAATCC 719

RESULT 13
BE780202
LOCUS 601468080F1 NIH_MGC_67 Homo sapiens cdna clone IMAGE:3871363 5',
DEFINITION mRNA sequence.
ACCESSION BE780202
VERSION BE780202.1 GI:10201400
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 911)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cdna Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9623 row: p column: 20
High quality sequence stop: 658.
Location/Qualifiers
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/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Library constructed by Life Technologies."

FEATURES
source

BASE COUNT 296 a 205 c 183 g 227 t

Query Match 13.7%; Score 584; DB 10; Length 911;
Best Local Similarity 94.7%; Pred. No. 1.1e-79;
Matches 714; Conservative 0; Mismatches 25; Indels 15; Gaps 10;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 26, 2003, 16:48:06 ; Search time 1027 Seconds
(without alignments)
11197.279 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4139.4	97.2	4215	22	AAS59388 Human cDNA encodin
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4	2958.8	69.5	6120	22	AAS59390 Mouse cDNA encodin
5	2862.6	67.2	6075	22	AAS59389 Mouse cDNA encodin
6	2732.2	64.1	6052	22	AAS59391 Mouse cDNA encodin
7	1674	39.3	3726	24	ABK63760 Rat sequence diffe
8	1648.4	38.7	3722	25	ACA56531 Human signalling p

9	1584	37.2	3768	24	ABK93499 Human cDNA differe
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14	1414.6	33.2	5261	22	AAK52651 Human polynucleoti
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26	495	11.6	2420	23	ABL17625 Drosophila melanog
27	434	10.2	489	22	AAS59462 Human KCC3a genom
28	397.2	9.3	2384	12	AAQ14633 Clone associated w
29	343	8.1	416	22	AAI89439 Human polynucleoti
30	335.2	7.9	1713	23	AAS91801 DNA encoding novel
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ALIGNMENTS

RESULT 1
AAS59394
ID AAS59394 standard; cDNA; 4260 BP.

XX AAS59394;

AC AAS59394;

XX 16-JAN-2002 (first entry)

DT Human cDNA encoding potassium-chloride cotransporter KCC3a.

DE Human; ss: potassium-chloride cotransporter; epilepsy; hypertension;
KW KCC; hypotensive; anticonvulsant; antianaemic; sickle-cell anaemia;
KW gene therapy.

XX Homo sapiens.

OS WO200179525-A2.

PN 25-OCT-2001.

PD 16-APR-2001; 2001WO-US12395.

PF 14-APR-2000; 2000US-197350P.

PR (UYVA-) UNIV VANDERBILT.

PA (GAMB/) GAMBA G.

PI Gamba G, Mount DB, Delpire E, George AL;

XX WPI; 2001-611726/70.

DR P-PSDB; AAU39099.

XX New isolated and purified potassium-chloride cotransporter polypeptide
PT for detecting a modulator of potassium-chloride cotransporter that can
PT treat epilepsy, sickle cell anaemia, and hypertension -
XX
PS Claim 10; Page 291-298; 352pp; English.
XX
CC The invention relates to an isolated and purified, biologically active
CC KCC2, KCC3, or KCC4 potassium-chloride cotransporter polypeptide
CC and polynucleotides encoding them. KCC and the nucleic acid encoding KCC
CC are used to produce an antibody against KCC, which can be used to detect
CC KCC. The antibody and nucleic acid are used in kits to detect KCC and
CC the nucleic acid encoding KCC. KCC and nucleic acid encoding it are used
CC to screen for candidate substances that can modulate the activity of KCC.
CC KCC and the nucleic acid encoding it can be used to modulate potassium-
CC chloride cotransport in a vertebrate. Therapeutic compositions
CC comprising modulators of the activity of KCC (preferably antibodies or
CC antisense oligonucleotides) are used to treat epilepsy, sickle cell
CC anaemia, and hypertension (also via gene therapy using the KCC
CC polynucleotide). The present sequence encodes a KCC of the invention.
XX
SQ Sequence 4260 BP; 1165 A; 974 C; 972 G; 1146 T; 3 other;

Query Match 99.9%; Score 4257; DB 22; Length 4260;
Best Local Similarity 100.0%; Pred. No. 0;
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QY 3721 TTCTGTACACATCATACTGAACTCTGATGAGCTGAGCCTCAAGTACCTGTGTAAAAGAG 3780
DB 3721 TTCTGTACACATCATACTGAACTCTGATGAGCTGAGCCTCAAGTACCTGTGTAAAAGAG 3780
QY 3781 CTCCCATCTGATCTGAGTCAATACAGAAAAGCAAAATTTCCCTCAACATCAGAACAAAT 3840
DB 3781 CTCCCATCTGATCTGAGTCAATACAGAAAAGCAAAATTTCCCTCAACATCAGAACAAAT 3840
QY 3841 GCTCAAGTCTTCAAGCCACTGCTGAGCAGTCAAGGCAAAATTTAGAAATTAACCAAGCTGA 3900
DB 3841 GCTCAAGTCTTCAAGCCACTGCTGAGCAGTCAAGGCAAAATTTAGAAATTAACCAAGCTGA 3900
QY 3901 GCCAATAAATGAATTTGGTAAAAGGATGCTAGAAATTTCAACTGAAGAAAAGCAAGCTC 3960
DB 3901 GCCAATAAATGAATTTGGTAAAAGGATGCTAGAAATTTCAACTGAAGAAAAGCAAGCTC 3960
QY 3961 AAGTACGTATTTACGATTAAGATGAATCTCAGAAAGTCAATGTTTCAATGTTGACACTGTG 4020

Db 3961 AAGTACGTATTAGCATTAAAGATGAATCTCAGAAGTCATGGTTCATGTTGACACTGTG 4020
Qy 4021 AGGATAACAACATAGAGACAGCTTCATCTTACTAAAGAAATTTATGTCGAAGTATATTTGGA 4080
Db 4021 AGGATAACAACATAGAGACAGCTTCATCTTACTAAAGAAATTTATGTCGAAGTATATTTGGA 4080
Qy 4081 CCTATTATCCTCGCAAGCCAAAGATGCAAAACATTTTATGCTATATTTCTTTAGTATACC 4140
Db 4081 CCTATTATCCTCGCAAGCCAAAGATGCAAAACATTTTATGCTATATTTCTTTAGTATACC 4140
Qy 4141 CACTGCTGTAATTTTATATTAGGATGATCTTAACCTTGAACATGCGCTGAGCTCTACTTCTT 4200
Db 4141 CACTGCTGTAATTTTATATTAGGATGATCTTAACCTTGAACATGCGCTGAGCTCTACTTCTT 4200
Qy 4201 CAAAACATCCCCCAAAATACAGATTTTAAATATCCAAAAAATTTTAAAAA 4260
Db 4201 CAAAACATCCCCCAAAATACAGATTTTAAATATCCAAAAAATTTTAAAAA 4260

RESULT 2
AAS59388
ID AAS59388 standard; cDNA; 4215 BP.
XX
AC AAS59388;
XX
DT 16-JAN-2002 (first entry)
XX
XX Human cDNA encoding KCC3a lacking exon 2.
DE Human; ss; potassium-chloride cotransporter; epilepsy; hypertension;
KW KCC; hypotensive; anticonvulsant; antianaemic; sickle-cell anaemia;
KW gene therapy.
XX
XX Homo sapiens.
OS
XX WO200179525-A2.
PN
XX 25-OCT-2001.
XX
XX 16-APR-2001; 2001WO-US12395.
PF
XX 14-APR-2000; 2000US-197350P.
PR
XX (UYVA-) UNIV VANDERBILT.
PA (GAMB/) GAMB G.
XX
XX Gamba G, Mount DB, Delpire E, George AL;
PI
XX WPI; 2001-611726/70.
DR
XX P-PSDB; AAU39093.
XX
XX New isolated and purified potassium-chloride cotransporter polypeptide
PT for detecting a modulator of potassium-chloride cotransporter that can
PT treat epilepsy, sickle cell anaemia, and hypertension -
XX
XX Claim 10; Page 217-224; 352pp; English.
PS
XX The invention relates to an isolated and purified, biologically active
CC KCC2, KCC3, or KCC4 potassium-chloride cotransporter polypeptide
CC and polynucleotides encoding them. KCC and the nucleic acid encoding KCC
CC are used to produce an antibody against KCC, which can be used to detect
CC KCC. The antibody and nucleic acid are used in kits to detect KCC and
CC the nucleic acid encoding KCC. KCC and nucleic acid encoding it are used
CC to screen for candidate substances that can modulate the activity of KCC.
CC KCC and the nucleic acid encoding it can be used to modulate potassium-
CC chloride cotransport in a vertebrate. Therapeutic compositions
CC comprising modulators of the activity of KCC (preferably antibodies or
CC antisense oligonucleotides) are used to treat epilepsy, sickle cell
CC anaemia, and hypertension (also via gene therapy using the KCC
CC polynucleotide). The present sequence encodes a KCC of the invention.
XX
XX Sequence 4215 BP; 1150 A; 961 C; 962 G; 1139 T; 3 other;
SQ

Query Match 97.2%; Score 4139.4; DB 22; Length 4215;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 4208; Conservative 0; Mismatches 5; Indels 47; Gaps 2;
Qy 1 TGAGTAGAAGTATTCTTAGTGTGGGCTTTTGTGTGGTGTGAATCAAGGTTATTGAAATG 60
Db 1 TGAGTAGAAGTATTCTTTAGTGTGGGCTTTTGTGTGGTGTGAATCAAGGTTATTGAAATG 60
Qy 61 TGTATTATTTTCAAGTTATCTTTTGTATTGTCAGTCAAAAGTAGCTAGCTTAAGAGGAAGAT 120
Db 61 TGTATTATTTTCAAGTTATCTTTTGTATTGTCAGTCAAAAGTAGCTAGCTTAAGAGGAAGAT 120
Qy 121 TTTGCGAGGTTTCCCCCACTTTTGTCTTAAAGAAACAAAATGATCCTCCAGAAA 180
Db 121 TTTGCGAGGTTTCCCCCACTTTTGTCTTAAAGAAACAAAATGATCCTCCAGAAA 180
Qy 181 CCACACCAAGATGGCTTCAGTTCGGTTCATGGTGTGACACCCGACCAAGATCGATGATTC 240
Db 181 CCACACCAAGATGGCTTCAGTTCGGTTCATGGTGTGACACCCGACCAAGATCGATGATTC 240
Qy 241 CAGGTTTGTGACACACAGTCCGGACNTCAGCTCTCGATCTAGTTCCTCCGAGTAAAGATT 300
Db 241 CAGGTTTGTGACACACAGTCCGGACNTCAGCTCTCGATCTAGTTCCTCCGAGTAAAGATT 300
Qy 301 GCTCCCGGAAAGCGTGCCTGAAACAAGCCGGAGTGAGCCTATGAGTGAGATGTCTGGGG 360
Db 301 GCTCCCGGAAAGCGTGCCTGAAACAAGCCGGAGTGAGCCTATGAGTGAGATGTCTGGGG 360
Qy 361 CCACACATTCCTGCGCAACTGTTGACATGATGACCCAGTGACCGGAGTCTTCAACCCC 420
Db 361 CCACACATTCCTGCGCAACTGTTGACATGATGACCCAGTGACCGGAGTCTTCAACCCC 420
Qy 421 AGGATGTCATCGAGGACCTGAGTCAGACTCCATCACAGGGGAACACAGCCAACTGTTAG 480
Db 421 AGGATGTCATCGAG- - - - -G 435
Qy 481 ACGACGGACATAAGAAAGCTCGAAATGCTTATCTCAATAATTTCCAATTTATGAAGAGGAG 540
Db 436 ACGACGGACATAAGAAAGCTCGAAATGCTTATCTCAATAATTTCCAATTTATGAAGAGGAG 495
Qy 541 ATGAATATTTTGAATAAAATTTGGCACTCTTTGAGGAAGAAATGGACACAGACCGAAGG 600
Db 496 ATGAATATTTTGAATAAAATTTGGCACTCTTTGAGGAAGAAATGGACACAGACCGAAGG 555
Qy 601 TGTCTTCCCTCTCAACCGCATGGCCAATTTACACTTAATCTGACTCAAGGAGCAAGGAAC 660
Db 556 TGTCTTCCCTCTCAACCGCATGGCCAATTTACACTTAATCTGACTCAAGGAGCAAGGAAC 615
Qy 661 ATGAAGAGCGAGAAAAACATCACTGAAGGAAAAAGAACCCACCAAGACCCCCCAATGG 720
Db 616 ATGAAGAGCGAGAAAAACATCACTGAAGGAAAAAGAACCCACCAAGACCCCCCAATGG 675
Qy 721 GTACCTTCATGGGTGCTACCTCCCATGCTTACAAAAATATTTTGGAGTATCTTTT 780
Db 676 GTACCTTCATGGGTGCTACCTCCCATGCTTACAAAAATATTTTGGAGTATCTTTT 735
Qy 781 TACGCTTTACATGGGTGGTGGGCACAGCTGGAGTTCTTCAGGCTTTTTCGAATTTGCTTTA 840
Db 736 TACGCTTTACATGGGTGGTGGGCACAGCTGGAGTTCTTCAGGCTTTTTCGAATTTGCTTTA 795
Qy 841 TCTGCTGCTGTGTAACAATGTTGACTGTCTATCTCCATGAGTGCCATTTGCCACTAATGGAG 900
Db 796 TCTGCTGCTGTGTAACAATGTTGACTGTCTATCTCCATGAGTGCCATTTGCCACTAATGGAG 855
Qy 901 TGGTGCCAGCTGGGGGCTCATACTTTATGATTTTCCCGGCACTGGGCCAGAGTTTGGTG 960
Db 856 TGGTGCCAGCTGGGGGCTCATACTTTATGATTTTCCCGGCACTGGGCCAGAGTTTGGTG 915
Qy 961 GGGCTGTTGGGCTCTGCTTTTATCTTGGTACCACATTTTGACAGCAGCATGTACATCCTTG 1020
Db 916 GGGCTGTTGGGCTCTGCTTTTATCTTGGTACCACATTTTGACAGCAGCATGTACATCCTTG 975

Db 3136 TATCAAAAACAGAGCGAGACAGAGAGCCAAATTTGGTGAAGACCCAACTCAATGCTAC 3195
Qy 3241 GATTGACAGCAATGGCTCTGTATGAGGACGAAGAGACAGAAACCTTATCAGGAGAGGTGC 3300
Db 3196 GATTGACAGCAATGGCTCTGTATGAGGACGAAGAGACAGAAACCTTATCAGGAGAGGTGC 3255
Qy 3301 ACATGACTTTGGACAAAGACAAGTACATGGCATCCGGGGGACAAAGGCAAGTCAATGG 3360
Db 3256 ACATGACTTTGGACAAAGACAAGTACATGGCATCCGGGGGACAAAGGCAAGTCAATGG 3315
Qy 3361 AAGGATTCAGGACCTGCTTACATGCTGTCGGACCAAGTCCAAATGTGAGCGGATGCATA 3420
Db 3316 AAGGATTCAGGACCTGCTTAAACATGCTGTCGGACCAAGTCCAAATGTGAGCGGATGCATA 3375
Qy 3421 CAGCAGTGAACCTCAACGAGGTTATAGTTAAACAAGTCCCATGAAGCAAGAGCTGTTTAT 3480
Db 3376 CAGCAGTGAANNTCAACGAGGTTATAGTTAAACAAGTCCCATGAAGCAAGAGCTGTTTAT 3435
Qy 3481 TGAATATGCCAGGGCCACCCCGAAACCTTGAGGGTGATGAAACCTACATGGAGTTCCTAG 3540
Db 3436 TGAATATGCCAGGGCCACCCCGAAACCTTGAGGGTGATGAAACCTACATGGAGTTCCTAG 3495
Qy 3541 AGGTGCTTACGAGGACCTAGAGCGAGTCTTACTTGTCCGGGTGGTGCAGTGAAGTGA 3600
Db 3496 AGGTGCTTACGAGGACCTAGAGCGAGTCTTACTTGTCCGGGTGGTGGCAGTGAAGTGA 3555
Qy 3601 TCACCATTTTATCATAACTACTCTGAATGACGCTGTGACCTGTTTTCTTAAAGGCC 3660
Db 3556 TCACCATTTTATCATAACTACTCTGAATGACGCTGTGACCTGTTTTCTTAAAGGCC 3615
Qy 3661 TAGCTCTCCATGGAAGTCCAGCTCATTTACTACCACTCCCACTCAACTAGAGGCTGTG 3720
Db 3616 TAGCTCTCCATGGAAGTCCAGCTCATTTACTACCACTCCCACTCAACTAGAGGCTGTG 3675
Qy 3721 TTCTGTACATCATACTGAACCTTTGTATGAGCTGAGCCTCAAGTACCTGTGTAAAGAG 3780
Db 3676 TTCTGTACATCATACTGAACCTTTGTATGAGCTGAGCCTCAAGTACCTGTGTAAAGAG 3735
Qy 3781 CTCCCATCTGATCTGAGTCATTTACAGAAAGCAAAATATTCCTCAACATCAGACAT 3840
Db 3736 CTCCCATCTGATCTGAGTCATTTACAGAAAGCAAAATATTCCTCAACATCAGACAT 3795
Qy 3841 GCTCAAGTCTTTCAAGCCCACTGTCTGAGCAGTCAAAAGGCAAAATTTAGAATTAACAAGCTGA 3900
Db 3796 GCTCAAGTCTTTCAAGCCCACTGTCTGAGCAGTCAAAAGGCAAAATTTAGAATTAACAAGCTGA 3855
Qy 3901 GCCAATAATGAATTTGGTAAAGGGATGCTAGAAATTTCACTGAAGAAAAAGCAAGTC 3960
Db 3856 GCCAATAATGAATTTGGTAAAGGGATGCTAGAAATTTCACTGAAGAAAAAGCAAGTC 3915
Qy 3961 AAGTACGTATTCAGCAATTAAGATGAATCTCAGAGCTCATGTTCAATGTTGACACTGTG 4020
Db 3916 AAGTACGTATTCAGCAATTAAGATGAATCTCAGAGCTCATGTTCAATGTTGACACTGTG 3975
Qy 4021 AGGATAACAACCTAGACAGCTTCATCTTACTAAAGAAATTTATGGTCAAGTATATTGGA 4080
Db 3976 AGGATA - CACTAGACAGCTTCATCTTACTAAAGAAATTTATGGTCAAGTATATTGGA 4033
Qy 4081 CCTATTATCTCTGGCAAGCAAGATGCAACATTTTTTTTATAGCTATATTTCTTTAGTATACC 4140
Db 4034 CCTATTATCTCTGGCAAGCAAGATGCAACATTTTTTTTATAGCTATATTTCTTTAGTATACC 4093
Qy 4141 CACTGCTGTAATTTTATATTAGGATACTACTTTGAACATGGCTGCGCTCTACTTCTT 4200
Db 4094 CACTGCTGTAATTTTATATTAGGATACTACTTTGAACATGGCTGCGCTCTACTTCTT 4153
Qy 4201 CAAAAACATCCCCCAAAATACCAGATTTTAAATATCCAAAAAATAAAAAAAAAAAAAA 4260
Db 4154 CAAAAACATCCCCCAAAATACCAGATTTTAAATATCCAAAAAATAAAAAAAAAAAAAA 4213

ID ABA09035 standard; cDNA; 3367 BP.
XX AC ABA09035;
XX DT 11-JAN-2002 (first entry)
XX DE Human K/Cl cotransporter homologue-encoding cDNA, SEQ ID NO:811.
DE KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; actin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnery; antiulcer; ss.
XX OS Homo sapiens.
XX WO200157188-A2.
XX PN 09-AUG-2001.
XX PD 05-FEB-2001; 2001WO-US03800.
XX PF 03-FEB-2001; 2000US-0496914.
XX PR 27-APR-2000; 2000US-0560875.
XX XX (HYSE-) HYSEQ INC.
XX XX Tang YT, Liu C, Drmanac RT;
XX WPI: 2001-457740/49.
XX P-PSDB; ABB11791.
XX PT Human proteins and DNA encoding sequences useful for preventing,
XX treating or ameliorating a medical condition in a mammalian subject
XX e.g. arthritis and cancer -
XX Claim 1: Page 717-718; 1963pp; English.
XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
XX sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
XX invention also relates to vectors and recombinant host cells comprising a
XX nucleotide of the invention, methods of producing the novel polypeptides,
XX antibodies against the polypeptides, methods of detecting the nucleotides
XX or polypeptides in a sample, and methods of identifying compounds which
XX bind to polypeptides of the invention. Although novel, many of the
XX polypeptides of the invention have homology to known proteins, thereby
XX giving an insight into their probable biological activities, and hence
XX potential therapeutic applications. The polypeptides of the invention may
XX have various activities, including cytokine, cell proliferation or cell
XX differentiation activities; stem cell growth factor activity;
XX haematopoiesis regulatory activity; tissue growth activity;
XX immunomodulatory activity; activin- or inhibin-related activities;
XX chemotactic or chemokinetic activities; haemostatic, thrombotic or
XX thrombolytic activities; receptor or ligand activities; or may be
XX involved in oncogenesis; cancer cell proliferation or metastasis.
XX Depending on their biological activities, polypeptides and nucleotides of
XX the invention are useful for preventing, treating or ameliorating medical
XX conditions, e.g., by protein or gene therapy. Such conditions include
XX cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
XX disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
XX proliferative retinopathy, atherosclerosis, coronary heart disease,
XX arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
XX vascular growth. Polypeptides involved with tissue regeneration and
XX repair (or nucleic acids encoding them) may be used to promote wound
XX healing (e.g., of burns, incisions and ulcers), while those with

CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness.
CC auto-immune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a
CC novel human polypeptide of the invention.
XX
XX Sequence 3367 BP; 889 A; 775 C; 811 G; 892 T; 0 other;

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Query Match          74.0%; Score 3152.8; DB 22; Length 3367;
Best Local Similarity 99.8%; Pred. NO. 0;
Matches 3176; Conservative 0; Mismatches 4; Indels 2; Gaps 2
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435	Qy	GACCTGAGTCAGAACTCCATCACAGGGGAAACACAGCCAACTGTTAGACGACGACATAAG	494
186	Db	GACCTGAGTCAGAACTCCATCAGAGGGGAAACACAGCCAACTGTTAGACGACGACATAAG	245
		GACCTGAGTCAGAACTCCATCAGAGGGGAAACACAGCCAACTGTTAGACGACGACATAAG	245
495	Qy	AAAGCTCGAAATGCTTATCTCAATAATTCAAATTTATGAAGAAGGAGATGAATATTTTGAT	554
246	Db	AAAGCTCGAAATGCTTATCTCAATAATTCAAATTTATGAAGAAGGAGATGAATATTTTGAT	305
		AAAGCTCGAAATGCTTATCTCAATAATTCAAATTTATGAAGAAGGAGATGAATATTTTGAT	305
555	Qy	AAAAATTTGGCACTCTTTTGAGGAAGAAATGGACACACGACCGAAGGTGTCTTCCTCCTCCTC	614
306	Db	AAAAATTTGGCACTCTTTTGAGGAAGAAATGGACACACGACCGAAGGTGTCTTCCTCCTCCTC	365
		AAAAATTTGGCACTCTTTTGAGGAAGAAATGGACACACGACCGAAGGTGTCTTCCTCCTCCTC	365
615	Qy	AACCGCATGCCCAATTACACTAATCTGACTCAAGGAGCAAAAGGACAATGAAGAGGCGAGAA	674
366	Db	AACCGCATGCCCAATTACACTAATCTGACTCAAGGAGCAAAAGGACAATGAAGAGGCGAGAA	425
		AACCGCATGCCCAATTACACTAATCTGACTCAAGGAGCAAAAGGACAATGAAGAGGCGAGAA	425
675	Qy	AACATCACTCAAGGGGAAAAGAACCCACCAAGACCCCCAAAATGGGTGACTCTCATGGGT	734
426	Db	AACATCACTCAAGGGGAAAAGAACCCACCAAGACCCCCAAAATGGGTGACTCTCATGGGT	485
		AACATCACTCAAGGGGAAAAGAACCCACCAAGACCCCCAAAATGGGTGACTCTCATGGGT	485
735	Qy	GTCTAGCTCCCATGTCTTACAAAATATTTTTGGAGTGATCTCTTTTTACGCTTACATGG	794
486	Db	GTCTAGCTCCCATGTCTTACAAAATATTTTTGGAGTGATCTCTTTTTACGCTTACATGG	545
		GTCTAGCTCCCATGTCTTACAAAATATTTTTGGAGTGATCTCTTTTTACGCTTACATGG	545
795	Qy	GTGGTGGGACAGCTGGAGTCTTTCAGGCTTTTTCGAATTCCTTATCTGCTGCTGCTGT	854
546	Db	GTGGTGGGACAGCTGGAGTCTTTCAGGCTTTTTCGAATTCCTTATCTGCTGCTGCTGT	605
		GTGGTGGGACAGCTGGAGTCTTTCAGGCTTTTTCGAATTCCTTATCTGCTGCTGCTGT	605
855	Qy	ACAAATGTTGACTGCTATCTCCATGAGTGCCATATGCCACTAAATGAGAGTGGTGCCAGCTGGG	914
606	Db	ACAAATGTTGACTGCTATCTCCATGAGTGCCATATGCCACTAAATGAGAGTGGTGCCAGCTGGG	665
		ACAAATGTTGACTGCTATCTCCATGAGTGCCATATGCCACTAAATGAGAGTGGTGCCAGCTGGG	665
915	Qy	GGCTCATACTTTATGATTTCCCGGGCACTGGGCGCCAGAGTTGGTGGGGCTGTTGGCCTC	974
666	Db	GGCTCATACTTTATGATTTCCCGGGCACTGGGCGCCAGAGTTGGTGGGGCTGTTGGCCTC	725
		GGCTCATACTTTATGATTTCCCGGGCACTGGGCGCCAGAGTTGGTGGGGCTGTTGGCCTC	725
975	Qy	TGCTTTTATCTTGATACCAATTTGCAGCAGCCATGATACCTCTTGTTGGTGCCATTTGAATC	1034
726	Db	TGCTTTTATCTTGATACCAATTTGCAGCAGCCATGATACCTCTTGTTGGTGCCATTTGAATC	785
		TGCTTTTATCTTGATACCAATTTGCAGCAGCCATGATACCTCTTGTTGGTGCCATTTGAATC	785
1035	Qy	TTTTCTGCTATATCTGTCCTCCCGAGCTGCCATCTTTTCAAGTATGATACGCACTCAAGGAA	1094
786	Db	TTTTCTGCTATATCTGTCCTCCCGAGCTGCCATCTTTTCAAGTATGATACGCACTCAAGGAA	845
		TTTTCTGCTATATCTGTCCTCCCGAGCTGCCATCTTTTCAAGTATGATACGCACTCAAGGAA	845
1095	Qy	TCAGCAGCCATGCTAAATAACATGCGTGTCTACGGGACAGCTTCTTGGTGCTTATGGGTA	1154
846	Db	TCAGCAGCCATGCTAAATAACATGCGTGTCTACGGGACAGCTTCTTGGTGCTTATGGGTA	905
		TCAGCAGCCATGCTAAATAACATGCGTGTCTACGGGACAGCTTCTTGGTGCTTATGGGTA	905
1155	Qy	TTAGTGGTATTTATCGGCGTAGCTATGTGAAACAAAGTTTGCCTCANTTTTCTTGGCCTGT	1214
906	Db	TTAGTGGTATTTATCGGCGTAGCTATGTGAAACAAAGTTTGCCTCANTTTTCTTGGCCTGT	965
		TTAGTGGTATTTATCGGCGTAGCTATGTGAAACAAAGTTTGCCTCANTTTTCTTGGCCTGT	965
1215	Qy	GTCAATGTGTCCATCTTTGGCCATCTATGTCTGGAGCCATCAAGTCTTCTTTGTCTCTCCA	1274
966	Db	GTCAATGTGTCCATCTTTGGCCATCTATGTCTGGAGCCATCAAGTCTTCTTTGTCTCTCCA	1025
		GTCAATGTGTCCATCTTTGGCCATCTATGTCTGGAGCCATCAAGTCTTCTTTGTCTCTCCA	1025

QY 162 AAAATGTCATCTCCAGAAACACCAACAGATGGCTTCAGTTGCGTTTCATGTTGACACCG 221
DB 1 AAAATGTCATCTCCAGAAACACCAACAGATGGCTTCAGTTGCGTTTCATGTTGACACCA 60
QY 222 ACAAGATCGATGACATTCAGGTTTGTCCAGACACCAAGTCCGGAACNTCAGCTCTCGATCT 281
DB 61 ACTAAGATTGATGACATTCAGGTTTGTCCAGACACCAAGTCCGGAACNTCAGCTCTCGGTC 120
QY 282 AGTTCCCGAGTAAGATTAGCTCCCGGAAAGGTCCTGAAACCAAGCCGAGTAGGCT 341
DB 121 AGTTCTCGAGTAAGATTAGCTCCCGGAAAGGTCCTGAAACCAAGCCGAGTAGGCT 180
QY 342 ATGAGTGAGATCTCTGGGSCCAACCTTCGCTGGCAACTGTGCACTGGATCCACCCAGT 401
DB 181 ATGACGGAACTCTCTGGGCTACTACTCTCTGGCAACTGTGCACTGGATCCCTCCAGT 240
QY 402 GACCGGACTCTTCAACCCAGGATGTCATCGAGGACCTGAGTCAGAACTCCATCACAGGG 461
DB 241 GACCGGACTCTTCAACCCAGGATGTCATCGAGGACCTGAGTCAGAACTCCATCACAGGG 300
QY 462 GAAACAGGCAACTGTTAGACGACGCAATAGAAAGCTCGAAATGCTTATCTCAATAAT 521
DB 301 GAGCAAGCCAGCTGTTAGATGACGGCCATAAAGGCGGAAATGCTTATCTCAATAAT 360
QY 522 TCCAAATTATGAAGAGGAGATGAATAATTTGATTAATAATTTGGCACTCTTTGAGGAAGNA 581
DB 361 TCCAACTATGAAGAGGAGAGCAATAATTTGATTAATAATTTGGCACTCTTTGAGGAAGNA 420
QY 582 ATGGACACGACGACCAAGGTCCTTCCCTCCTCAACCGCATGGCCAAATTAACAATACTG 641
DB 421 ATGGACACGACGACCAAGGTCCTTCTCTCAACCGCATGGCCAAATTAACAATACTG 480
QY 642 ACTCAAGGAGCAAGGAAATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 701
DB 481 ACACAAGGAGCAAGGAAATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
QY 702 ACCAAGACCCCAATGGGTACCTTCATGGGTGTCACCTCCCATGTCACAAATATT 761
DB 541 ACCAAGACCCCAATGGGTACCTTCATGGGTGTCACCTCCCATGTCACAAATATT 600
QY 762 TTTGAGTGATCTCTTTTATAGCCCTATACATGGGTGGGACACAGCTGGAGTTCTTCAG 821
DB 601 TTTGAGTGATCTCTTCTCTGGTCTTAACCTGGGTAGTGGGAAAGCTGGATCTTCAG 660
QY 822 GCTTTTGGCAATGTCCTTATCTGCTGCTGTGACAAATGTTGACGTCTATCTCCATGAGT 881
DB 661 GCTTTTGGCAATGTCCTTATCTGCTGCTGTGACAAATGTTGACGTCTATCTCCATGAGC 720
QY 882 GCCATTGCCACTAATGGAGTGGCCAGCTGGGGCTCATCTTTATCATTTCCCGGCA 941
DB 721 GCCATTGCCACTAATGGAGTGGCCAGCTGGGGCTCATCTTCATGATTTCCAGAGCC 780
QY 942 CTGGGCCCCAGAGTTTGGTGGGCTGTGGCCCTCTGCTTTTATCTTTGGTACACATTTGCA 1001
DB 781 CTGGGCCCCAGAGTTTGGCGGGCTGTAGCCCTCTGCTTTTATCTTTGGCACCAATTTGCA 840
QY 1002 GCAGCCATGTATCTTTGGTGCCATTCGAATCTTTCTGGTCTATATGCTCCCGGAGCT 1061
DB 841 GCAGCCATGTATCTTTGGTGCCATTCGAATCTTTCTGGTATATATGTTCCCGGAGCT 900
QY 1062 GCCATCTTTACAGTATGAGCACTCAAGGAATCAGGAGCCATGCTAAATAACATGGCT 1121
DB 901 GCCATCTTTACAGTATGAGCACTCAAGGAATCAGGAGTATGCTGAAACAATGCGC 960
QY 1122 GTCTACGGCAGAGCTTCTTGGTCTTATGTTATGTTAGTGTATTTATCGGGGTAGCTAT 1181
DB 961 GTCTATGGTACAGCTTCTTGGTCTTATGTTATGTTAGTGTATTTATCGGGGTAGCTAT 1020
QY 1182 GTGAACAAGTTTGGCTCANTTTTCTGGCCCTGTGTGCTTGTGCTCATCTTTGGCCATCTAT 1241
DB 1021 GTGAATAAGTTTGGCTCACTCTTCTGGCCCTGTGTGCTTGTGCTCATCTTTGGCTATCTAT 1080
QY 1242 GCTGAGGCCATCAAGTCTTTCTTCTCTCTCCACACTTCCCGGCTGTCATGCTGGGTAAAC 1301

DB 1081 GCTGTGCCATCAAGTCTTTCTTCTCCACACACTTCCCGGCTGTATGCTGGGCAAC 1140
QY 1302 CGCACTCTTTTCATCAAGACACATTCAGCTTTGCTCTAAGACCAAGGAAATTAACAACATG 1361
DB 1141 CGTACCTCTGTCTCATCAAGACACCTTGACATTTGCTCTAAGACCAAGGAGTTGACAACTG 1200
QY 1362 ACAGTCCCATCAAAAGTTATGGGATCTTCTGTGTAACCTGAGTCAATTTTTCAATGCCACC 1421
DB 1201 ACAGTACCATCAAAAGTTATGGGATCTTCTGCAACTCGAGTCAGTCTTTAATGCCACC 1260
QY 1422 TGTGATGATACTTTGTTTCAAACTGCTACTCTCAATCAAGGCAATTTCCAGGGTTGGCT 1481
DB 1261 TGTGATGATACTTTGTTTCAAACTGCTACTCTCAATCAAGGCAATTTCCAGGGTTGGCT 1320
QY 1482 AGTGATTAATAATACAGAGAATCTTTGGAGTAATTTACCTACCAAGGAGAGATCATCGAA 1541
DB 1321 AGTGATTAATAATCTGGAATACTTTGGAGTAATTTATTTACCAAGGAGTGAATAATTGNA 1380
QY 1542 AAGCTTTGAGCAAACTCTTCTGATGCTTGAAGAGCTTTAAACCATGAATAATGTTCTTGT 1601
DB 1381 AAGCCATCAGCAAGTCTATCTGATGCTTAGGCAACTTAAACCATGAATAATGTTCTTGT 1440
QY 1602 GACATCACCACTCTTTCAGCTTCTGCTGGTGGGAATCTTCTTCCCTCTGTTACAGGTATC 1661
DB 1441 GATATCACCACTCTTTCAGCTTCTGCTGGTGGGATCTTCTTTCCTCGCTCACAGGTATC 1500
QY 1662 ATGGCTGATCAAAACAGATCTGGAGATCTGAAAGATGCTCAGAAAGTCTATTTCCGATCGT 1721
DB 1501 ATGGCTGGTCAAAACAGATCTGGAGATCTGAAAGATGCCAGAAAGTCTATTTCCCATGGG 1560
QY 1722 ACTATCTTGGCATCTTGACCACTCTCTTGTGTTTATTTAAGCAATGTTGCTCTTTTGGT 1781
DB 1561 ACCATCTTGGCATCTTGACCACTCTTGTGATTTAAGCAATGTTGCTCTTTTGGT 1620
QY 1782 GCATGATTTGAAGGGTGTGTTCTCAGAGACAGTTCGCTGATGCTGTGAAAGGTAATTTG 1841
DB 1621 GCATGATTTGAAGGAGTGTGTTCTCAGAGACAAATTTGGGGATGCTGTAAAAGGGAATTTG 1680
QY 1842 GTGATAGCACCTTATCTTGGCCATCCCATGGGTGATTGTTATTTGGCTCTTCTTTTCA 1901
DB 1681 GTTGTAGCACCTTATCTTGGCCATCCCGTGGGTGATCGTATTTGGCTCTTCTTTTCA 1740
QY 1902 ACATGTGGGCTGCACTTCAGAGCTTCAGAGCTTCAGAGGCTCAGAGGCTGCTCAAGCTATTGCC 1961
DB 1741 ACATGTGGGCTGGCTGCAGAGCTTCAGAGTGCCTCGCTCGCTGCTGAGCTATCGCC 1800
QY 1962 AAGGATAACATCATACCGTTCTGAGGTTTGGCCACAGCAAGCAATGGGGAACT 2021
DB 1801 AAGGATAACATCATACCTTCTTAGGGTTTGGTCTCAGCAAGGCTAATGGGGAACT 1860
QY 2022 ACCTGGCTTTTACCTTAACTGCTGCCATTCAGAGCTTGGAACTACCTATTCCTCCCTG 2081
DB 1861 ACCTGGCTTTTACCTTAACTGCTGCCATTCAGAGCTGGGAATCTCATCGCTCCCTG 1920
QY 2082 GATCTGTGSCCCCAATCTTTTCAATGTTTTCTCATGTTTACCTCTTTGTAAACTTG 2141
DB 1921 GATCTGTGSCCCCAATCTTTTCCATGTTTTCTCATGTTTACCTCTTTGTGAACCTG 1980
QY 2142 GCATGCTCTTGCNAACATTTCTTCGAACACCCAACTGGAGACCCCGATTCGCTACTAC 2201
DB 1981 GCTTGTGCTTGCNAACATTTGCTGCAACCCCACTGGAGGCTCGAATTCGCTATAT 2040
QY 2202 CATTTGGSCCTTCTTTTATGGGAATGAGTATCTGCTGCTGCTGATGTTTCATTTCTCC 2261
DB 2041 CATTTGGSCCTTCTTTTATGGGAATGAGTATCTGCTAGCTCTGATGTTTCATTTCT 2100
QY 2262 TGGTATTATGCCATTTGAGCCATGGTAATAGCTGGTATGATCTACAAGTACATTTGAATAC 2321
DB 2101 TGGTATTATGCCATTTGAGCTATGGTAATAGCTGGCATGATCTACAAGTACATTTGAATAT 2160
QY 2322 CAAGGAGCTGAGAAAGATGGGTGATGGTATCCGTGGGCTGCTCCCTCAGTGCAGCCGG 2381

Db 2161 CAAGGGCTGAGAAAGATGGGGGATGGTATCCGTGGGCTGTCTCAGTGCAGCCCGC 2220
Qy 2382 TTTCGCTTTGCTTCGATTGGAGGAAGGACCTCCACACACTTAAACCTGAGAGCCCTCAGTTG 2441
Db 2221 TTTCGCTTTGCTTCGATTGGAGGAAGGACCTCCACACACTTAAACCTGAGAGCCCTCAGTTG 2280
Qy 2442 TTTCGCTTTGCTTCGATTGGAGGAAGGACCTCCACACACTTAAACCTGAGAGCCCTCAGTTG 2501
Db 2281 TTTCGCTTTGCTTCGATTGGAGGAAGGACCTCCACACACTTAAACCTGAGAGCCCTCAGTTG 2340
Qy 2502 GCTTCACAGCTCAAGAGCAAGAAAGGTTTCACTATTTGGGGCTCTGTATCGTGGGGAAC 2561
Db 2341 GCTTCACAGCTCAAGAGCAAGAAAGGTTTCACTATTTGGGGCTCTGTATCGTGGGGAAC 2400
Qy 2562 TTTCCTAGAGAACTAGCGTGAAGCTTTAGCTGTGAGCAGACCATTAAGCACCCTATGAG 2621
Db 2401 TTTCCTAGAGAACTAGCGTGAAGCTTTAGCTGTGAGCAGACCATTAAGCACCCTATGAG 2460
Qy 2622 GCAGAGAAAGTAAAGGATTTCTGCCAGCTGTGGTGGCGCCCAAGCTGAGAGAGGCAAT 2681
Db 2461 GCAGAGAAAGTAAAGGATTTCTGCCAGCTGTGGTGGCGCCCAAGCTGAGAGAGGCAAT 2520
Qy 2682 TCCCACTCATCAGTCACTGTGGCTTGGGGCATTAAGACACAACACAGTGGTGTGATGGC 2741
Db 2521 TCACACCTCATCAGTCACTGTGGCTTGGGGCATTAAGACACAACACAGTGGTGTGATGGC 2580
Qy 2742 TGGCCTAATGGCTGAGGCTCAAGAGCAAGATGCGCGGCTTGAAGACATTTATTTGGCACA 2801
Db 2581 TGGCCTAATGGCTGAGGCTCAAGAGCAAGATGCGCGGCTTGAAGACATTTATTTGGCACA 2640
Qy 2802 GTTCAGTGCACAACTGCTCCCATCTTGCACTGTGGTGGCTTAAACCAATCTCTCTTTT 2861
Db 2641 GTACAGTGCACAACTGCTCCCATCTTGCACTGTGGTGGCTTAAACCAATCTCTCTTTT 2700
Qy 2862 CCCAGCAATGTGGAGCAATTTCTGAGGCAACATTTGATGTGTGGTGGATGTGATGAT 2921
Db 2701 CCCAGCAATGTGGAGCAATTTCTGAGGCAACATTTGATGTGTGGTGGATGTGATGAT 2760
Qy 2922 GGGGGATGCTTATGCTATCCTACTTCTTCTGAAACAGCAAGGTGTGGGCAAGTGC 2981
Db 2761 GGGGGATGCTTATGCTATCCTACTTCTTCTGAAACAGCAAGGTGTGGGCAAGTGC 2820
Qy 2982 AGCATACCGATCTTACAGTAGCCCAATTTAGAGCAACAGTATCCAAATGAAGAGGAC 3041
Db 2821 AGCATACCGATCTTACAGTAGCCCAATTTAGAGCAACAGTATCCAAATGAAGAGGAT 2880
Qy 3042 CTAGGCACCTCTCTATATCACTTACGATGTAGGCGGAGGTAGAGTGTGTGAGATGAT 3101
Db 2881 CTGGCCACCTCTCTGTACCACTGCGCATTTGAGGCAAGGTGGAAGTGTGGAGATGCAC 2940
Qy 3102 GACAGTGATATACAGATATCTTACGAGCGCATTTGATGATGGAACAAAGGTCCCGAG 3161
Db 2941 GACAGTGATATCTGCTTATACATATGAGCGCACCTGATGATGAGCAGAGGTCCCGAG 3000
Qy 3162 ATGCTTCGGCAGATGCGGCTATCCAAAACAGAGCGAGCAGAGGCAACATTTGGTGA 3221
Db 3001 ATGCTTCGGCAGATGCGGCTATCCAAAACAGAGCGAGCAGAGGCAACAGTGTGAA 3060
Qy 3222 GACCGAACTCAATGCTACGATTTGACAGCATTTGGCTCTGTATGAGGACGAAGAGCAGAA 3281
Db 3061 GATCGAACTCAATGCTACGCTTGACAGCATTTGGCTCTGTATGAGGACGAAGAGCAGAA 3120
Qy 3282 ACCTATCAGGAGAGGTGCATGACTTTGAGCAAAAAGCAAGTATGATGCGATCCCGGGA 3341
Db 3121 ACCTATCAGGAGAGGTGCATGACTTTGAGCAAAAAGCAAGTATGATGCGATCCCGGGA 3180
Qy 3342 CAAAAGCGAAGTCAATGGAAGGATTTCCAGAGCTCTTAAACATGCTCGGACCACTCC 3401
Db 3181 CAAAAGCGAAGTCAATGGAAGGATTTCCAGAGCTCTTAAACATGCTCGGACCACTCC 3240
Qy 3402 AATGTGAGCGGATGATACAGAGTGAACCTCAACAGAGTTTATAGTTAACAGTCCCAT 3461
Db 3241 AATGTGAGCGGATGATACAGAGTGAACCTCAATGAAGTTATAGTTAACAGTCTCAT 3300

Qy 3462 GAACAAAGCTGGTTTATTGAATATGCCAGGGCCACCCGAAACCCCTGAGGGTGATGAA 3521
Db 3301 GAACAAAGCTGGTTTATTGAATATGCCAGGACCCCGGAAACCCCTGAGGGTGATGAA 3360
Qy 3522 AACTACATGGAGTTCTTAGAGGTCTTACGAGGGACTAGAGCGAGTCTTACTTGTCCGG 3581
Db 3361 AACTACATGGAGTTCTTAGAGGTCTTACGAGGGACTAGAGCGAGTCTTACTTGTCCGG 3420
Qy 3582 GGTGGTGGCAGTGAAGTGATCACCATTATTATCAACCTACTCTGAATGACCGTGTGA 3641
Db 3421 GGTGGTGGCAGTGAAGTGATCACCATTATTATCAACCTACTCTGAATGACCGTGTGA 3480
Qy 3642 CCTGTTTCTTAAAGGCTTACGCTCCCTCATGGAAGTGCCAGCTCATTACTACCACTCCC 3701
Db 3481 TCCGACTTCCCTAA---GACTCATGTCCTCATGGAGATAGTCTTTCTTACCACTCCC 3537
Qy 3702 ACTCAACTAGAGCTGTGTTTCTGTACATCATCTACTGAACCTTTGTAGTGAAGCTC 3761
Db 3538 ACTC-----TATTCTGCAGAGCTGAGCCCC 3563
Qy 3762 AAGTACCTGTGTAAGAGGCTCCCATCTGATCTGCAGTCTATTACAGAAAAGCAATATT 3821
Db 3564 ATCTATGCTCTT-----GGCTGCAACATGATCTGC---CATCCAGCAGAAACAAATAAT 3615
Qy 3822 CCCTCAACATCAGAACCAATGCTCAAGTCTTTCAAGCCACTGTCTGAGCAGTCAAAGGCAA 3881
Db 3616 CCCTCAA---CAGAAGATGCTCAAGTCTTAAAGCTATTTCTATGGCAGGAGGCA 3672
Qy 3882 ATTAGAATTAAACAAGCTGAGCCAA-----TAAATGAATTGG 3917
Db 3673 GTCAAAATTAAACAAGCTAAGCCAAAGGAAACCTTTTGGCACACAGAGGTAAATGAGTTAG 3732
Qy 3918 TAAAGGATGCTAGAAATTTCACTGAAGAAAAGCAAGTCAAGTACGTATTTCAGCAT 3977
Db 3733 TAAACATATGCTAGAAATTTAACTGGCAACAGAAAGCA----ATGTTTATATCTTAACAT 3788
Qy 3978 TAAAGATCAATCTCAGAGTCAATGTTCAATGTTGAC 4014
Db 3789 TCAGACAGTTTCAGAGACACCGGTCAGTGAGCAC 3825

RESULT 5

AAS59389
ID AAS59389 standard; cDNA; 6075 BP.

XX AAS59389;

XX 16-JAN-2002 (first entry)

XX Mouse cDNA encoding KCC3a lacking exon 2.

XX Mouse; ss; potassium-chloride cotransporter; epilepsy; hypertension;
KW KCC; hypotensive; anticonvulsant; antianaemic; sickle-cell anaemia;
KW gene therapy.

XX Mus sp..

XX WO200179525-A2.

XX 25-OCT-2001.

XX 16-APR-2001; 2001WO-US12395.

XX 14-APR-2000; 2000US-197350P.

XX (UYVA-) UNIV VANDERBILT.

XX (GAMB/) GAMBA G.

XX Gamba G, Mount DB, Delpire E, George AL;

XX WPI; 2001-611726/70.

DR P-PSDB; AAU39094.

1815 QY TTGCGTGATGCTGTGAAAGGTAAATTTGGTGTAGGCACCTTATCTTTGGCCATCCCATGG 1874
1816 DB TTTGGGATGCTGTAAAGGGAATTTGGTGTAGGCACCTTATCTTTGGCCATCCCATGG 1645
1817 QY GTGATGTTATTTGGTCTCTTTTCAACATGTGGGGTGGACTTCAGAGCCTCAAGGT 1934
1818 DB GTGATGTTATTTGGTCTCTTTTCAACATGTGGGGTGGACTTCAGAGCCTCAAGGT 1705
1935 QY GCACCGGCTGCTACAGCTATTGCCAAGGATAACATACATACCTTTCTTGAGGGTTTTT 1994
1936 DB GCGCCTCGGCTGCTGAGGCTATCGCCAAGGATAACATACATACCTTTCTTGAGGGTTTTT 1765
1995 QY GCGCAGCAAAAGCACTGCGGAACTGCTGCGGCTTTACTTTCTAACTGCTGCCATTGCA 2054
1996 DB GGTACAGCAAAAGCTAATGGGGAACCTACCTGGGCTTTACTTTCTAACTGCTGCCATTGCA 1825
2055 QY GAGCTTGGGAATCTCATTTGCCCTCCCTGGGATCTTTGGGCCCCAAATCTTTTCCATGTTTTT 2114
2056 DB GAGCTTGGGAATCTCATTTGCCCTCCCTGGGATCTCGTGGCCCCAAATCTTTTCCATGTTTTT 1885
2115 QY CTCATGCTTACTCTTTGTAACCTTGGCATGTGCTTGCCTTGCACCACTTACTTGCACACCC 2174
2116 DB CTCATGCTTACTCTTTGTAACCTTGGCATGTGCTTGCCTTGCACCACTTACTTGCACACCC 1945
2175 QY AACTGGAGACCCGATTCGCTACTACCACTTGGGCTTTCTTTTCAATGGGAATGAGTATC 2234
2176 DB AACTGGAGACCCGATTCGCTACTATTAATCACTGGGCTTTCTTTTCAATGGGAATGAGTATC 2005
2235 QY TGTCTGGCTCTGATGTTCAATTTCTTCTGGTATTAATGCAATTTGAGCCATGTAATAGCT 2294
2236 DB TGTCTGGCTCTGATGTTCAATTTCTTCTGGTATTAATGCAATTTGAGCCATGTAATAGCT 2065
2295 QY GGTATGATCTACAAGTACATTAATCAAGGAGCTGAGAAAGAAATGGGGGATGGTATC 2354
2296 DB GGTATGATCTACAAGTACATTAATCAAGGAGCTGAGAAAGAAATGGGGGATGGTATC 2125
2355 QY CGTGGGCTGCTCCTCAGTCAGCCCGGTTTGTCTTGTCTGATTTGGAGGAAGCACTCCA 2414
2356 DB CGTGGGCTGCTCCTCAGTCAGCCCGGTTTGTCTTGTCTGATTTGGAGGAAGCACTCCA 2185
2415 QY CACACTAAAACTGGAGGCTCAGTGTCTGATTAATCACTGAACTAGATGAAGACTTACAT 2474
2416 DB CACACTAAAACTGGAGGCTCAGTGTCTGATTAATCACTGAACTAGATGAAGACTTACAT 2245
2475 QY GTCAAGCATCTCGCTCCTCAGTGTCTGATTAATCACTGAACTAGATGAAGACTTACAT 2534
2476 DB GTCAAGCATCTCGCTCCTCAGTGTCTGATTAATCACTGAACTAGATGAAGACTTACAT 2305
2535 QY ATTGTGGGCTCTGTCATCGTGGGAACTTCTTAGAGAACTACGGTGAAGCTTTAGCTGCT 2594
2536 DB ATTGTGGGCTCTGTCATCGTGGGAACTTCTTAGAGAACTACGGTGAAGCTTTAGCTGCT 2365
2595 QY GAGCAGACCAATAAGCACCCTAATGGAGGAGAGAAAGTAAAGGATTTCTGCCAGCTGGTG 2654
2596 DB GAGCAGACCAATAAGCACCCTAATGGAGGAGAGAAAGTAAAGGATTTCTGCCAGCTGGTG 2425
2655 QY GTGGCCCGCAGCTGAGAGGGCAATTCACCTCATCCAGTCACTGCGCTTGGGGC 2714
2656 DB GTGGCCCGCAGCTGAGAGGGCAATTCACCTCATCCAGTCACTGCGCTTGGGGC 2485
2715 QY ATGAAGCACAACACGCTGATGGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 2774
2716 DB ATGAAGCACAACACGCTGATGGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 2545
2775 QY CGCGCTTGAAGACTTTTATTTGCAAGCTTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2834
2776 DB CGCGCTTGAAGACTTTTATTTGCAAGCTTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2605
2835 QY CTGGTGGCTTAAACATCTCTCTTTTCCAGCAATGTGGAGCAATTTTCTGAGGCAAC 2894
2836 DB CTGGTGGCTTAAACATCTCTCTTTTCCAGCAATGTGGAGCAATTTTCTGAGGCAAC 2665
2895 QY ATTGATGTGGTGGATTTGTCATGATGGGGGATGCTTATGCTACTACCATTTCTACTG 2954

2666 DB ATTGATGTGGTGGATTTGTCATGATGGGGCATGCTCATGCTATTACCGTTCTGCTG 2725
2955 QY AAAAGCAGCAGGTGTGGCGAAGTGCAGCATACGGATCTTTCACAGTAGCCCAATTAGAA 3014
2956 DB AAAAGCAGCAGGTGTGGCGAAGTGCAGCATACGGATCTTTCACAGTAGCCCAATTAGAA 2785
3015 QY GACAACTATCTCAAAATGAAGAAGCCTAGCAGCTTCTTATATCACTTACGCAATTGAG 3074
3016 DB GACAACTATCTCAAAATGAAGAAGCCTAGCAGCTTCTTATATCACTTACGCAATTGAG 2845
3075 QY GCGAGGTGAGAGTGTGGAGATGCATGACAGTGCATATATCAGCATATATCAGAGGCG 3134
3076 DB GCGAGGTGAGAGTGTGGAGATGCATGACAGTGCATATATCAGCATATATCAGAGGCG 2905
3135 QY ACTTTGATGATGGAACAAAGGTCCAGATGCTTGGGCATATGCGGCTGTCCAAAACAGAG 3194
3136 DB ACTTTGATGATGGAACAAAGGTCCAGATGCTTGGGCATATGCGGCTGTCCAAAACAGAG 2965
3195 QY CGAGACAGAGGACCAATTTGGTGAAGACCGAACTCAATGCTACGATTGACAGCAATT 3254
3196 DB CGAGACAGAGGACCAATTTGGTGAAGACCGAACTCAATGCTACGATTGACAGCAATT 3025
3255 QY GGCTCTGATGAGGACGAGACAGAACTTATCAGGAGAGGTGCATGATCTTTGGACA 3314
3256 DB GGCTCTGATGAGGACGAGACAGAACTTATCAGGAGAGGTGCATGATCTTTGGACC 3085
3315 QY AAAGCAAGTACATGCGTCCGAGCAGTCCAGGACAAAGAGTCAATGGAAGGATTCAGGAC 3374
3316 DB AAAGCAAGTACATGCGTCCGAGCAGTCCAGGACAAAGAGTCAATGGAAGGATTCAGGAC 3145
3375 QY CTGCTTAACATGCGTCCGAGCAGTCCAGTCAATGAGCGGATGCATACAGCAGTGAACCTC 3434
3376 DB CTGCTTAACATGCGTCCGAGCAGTCCAGTCAATGAGCGGATGCATACAGCAGTGAACCTC 3205
3435 QY AACGAGTATAGTTAAACAAGTCCCATGAAGCTTCTTGAATATGCAAGTGAAGG 3494
3436 DB AACGAGTATAGTTAAACAAGTCCCATGAAGCTTCTTGAATATGCAAGTGAAGG 3265
3495 QY CCACCCCGAAGCTTGAAGGATGAGAACTACATGGAAGTCTTCTAGAGTGTCTACCTGAG 3554
3496 DB CCACCCCGAAGCTTGAAGGATGAGAACTACATGGAAGTCTTCTAGAGTGTCTACCTGAG 3325
3555 QY GGACTAGAGCAGTCTTACTTGTCCGGGTGCTGAGTGAAGTGCATCACCATTATTTCA 3614
3556 DB GGACTAGAGCAGTCTTACTTGTCCGGGTGCTGAGTGAAGTGCATCACCATTATTTCA 3385
3615 QY TAACTTACTGAAATGACCGTCTTGAACCTTCTTAAAGGCTTCTTAAAGGCTTCTTCACTG 3674
3616 DB TAACTTACTGAAATGACCGTCTTGAACCTTCTTAAAGGCTTCTTCACTG 3442
3675 QY AAGTCCAGCTCATTTACTACCTCCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 3734
3676 DB AAGTCCAGCTCATTTACTACCTCCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 3473
3735 QY TACTGAACCTTGTAGCTGAGCTGAGCTCAAGTACCTGTGTAAAGAGCTCCCATCTGATCT 3794
3736 DB TACTGAACCTTGTAGCTGAGCTGAGCTCAAGTACCTGTGTAAAGAGCTCCCATCTGATCT 3523
3795 QY GCAGTCAATTACAGAAAAAGCAAAATATCCCTCAACATCAGAACTTCTTCAAGTCTTCA 3854
3796 DB GCAGTCAATTACAGAAAAAGCAAAATATCCCTCAACATCAGAACTTCTTCAAGTCTTCA 3577
3855 QY AGCCTGCTGAGCAGTCAAGGCAAAATAGAAATTAACAGCTGAGCCTCAAGGCTGAGCCTCA 3905
3856 DB AGCCTGCTGAGCAGTCAAGGCAAAATAGAAATTAACAGCTGAGCCTCAAGGCTGAGCCTCA 3637
3906 QY TAAATGAATTTGGTAAAGGATGCTAGAAATTTCACTGAAGAAAA 3950
3907 DB TAAATGAATTTGGTAAAGGATGCTAGAAATTTCACTGAAGAAAA 3697
3951 QY AAAGCAAGTCAAGTATTCAGCATTTAAAGATGAATCTCAGAGTCAATGTTCAATGT 4010
3952 DB AAAGCAAGTCAAGTATTCAGCATTTAAAGATGAATCTCAGAGTCAATGTTCAATGT

Db 3698 AAAGCA---ATGTTTATATCTAACATTCAGGACGAGTTTCAGAGACACGGGTCACTGA 3753

Qy 4011 TGAC 4014

Db 3754 GCAC 3757

RESULT 7

ABK63760

ID ABK63760 standard; cDNA; 3726 BP.

XX

AC ABK63760;

XX

DT 18-JUN-2002 (first entry)

XX

DE Rat sequence differentially expressed in response to a hepatotoxin #1667.

XX

Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;

KW

differential expression; centrilobular necrosis; steatosis.

XX

OS Rattus norvegicus.

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PN WO200210453-A2.

XX

PD 07-FEB-2002.

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PF 30-JUL-2001; 2001WO-US23872.

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PR 31-JUL-2000; 2000US-222040P.

XX

PR 02-NOV-2000; 2000US-244880P.

PR

PR 11-MAY-2001; 2001US-290029P.

PR

PR 15-MAY-2001; 2001US-290645P.

PR

PR 22-MAY-2001; 2001US-292336P.

PR

PR 06-JUN-2001; 2001US-295798P.

PR

PR 13-JUN-2001; 2001US-297457P.

PR

PR 19-JUN-2001; 2001US-298884P.

PR

PR 09-JUL-2001; 2001US-303459P.

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PA (GENE-) GENE LOGIC INC.

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PI Mendrick D, Porter MW, Johnson KR, Castle AL, Elashoff MR;

XX

DR WPI; 2002-241625/29.

XX

Pt Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells -

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Db	1011	GCTGTGGACTTTCTTCTGCCACAGCCCCAACCTTACTGCTGACTCCTGTGACCCCTACTT	1070
Qy	1436	TGTTTCAATAAAGTCACCTTCAATCCAGGGCAATCTCTGGATTGGCTAGTGGTATAATTAC	1495
Db	1071	CCTGCTCAACATGTGACAGAGTTCTTGCGATACCTGGGGCAGCTGCTGTGCTCCA	1130
Qy	1496	AGAGAACTTTTGGAGTAATTAACCTACCCAGGAGAGATCATCGAAAGCCCTTCAGCCAA	1555
Db	1131	GGAAACACCTGTGGAGTGTCTTACCTGGAGAAGGTGAGGTGTGGAGAAGCATGGGCTGCC	1190
Qy	1556	ATCTTCTGATGTCTTAGGCAGCTTAA-----CAATGAATATGTTCTTGTGACATCAC	1609
Db	1191	CTCCACAGATACCTTTGGCCTGAAGGAGAGCCGTGCTCTGTATGTGGTGGCCGACATCGC	1250
Qy	1610	CACCTCTCTCAGCTTCTCGTGGGAATCTTCTCCCTGATTAAGGTATCATGCTGG	1669
Db	1251	CACATCTTTCACGCTGCTGGTGGCATCTTTTCTCCCTCTGTAACAGGACATCATGGCTGG	1310
Qy	1670	ATCAACAGATCTGGAGATCTGAAAGATCTCAGAACTCTATTCGGAATGGTACTATCCT	1729
Db	1311	CTCAAAACCGTTCGGGGACCTCCGTGATGCTCAGAAGTCTATCCCTGTGGGGACCATCT	1370
Qy	1730	TGCGATCTGACACCTCTCTTGTATTTAAGCAATGTTGCTCTTTTGGTGGATGTAT	1789
Db	1371	GGCTATTTGTCACCACTTCACTCGTGTACTTCAAGCATGTGTATCTCTCGGTGCCGTGAT	1430
Qy	1790	TGAAGGGTGTCTTCAGAGACAAAGTTCGGTGTATGCTGTGAAGGTAAATTCGTGGTAGG	1849
Db	1431	CGAGGGTGTGGTCTCCGGACAAGTACGGGTATGGCGTCAGAGAACTCGTGGTAGG	1490
Qy	1850	CACCTTATCTTGGCCATCCCATGGGTGATGTTTATTTGGCTCCTTCTTTTCAACATGTGG	1909
Db	1491	CACCTTGGCTTGGCCTTCACTTGGGTATCGTGGTGGCTCTTCTTCTCAACATGTGG	1550
Qy	1910	GGCTGACCTTCAGAGCTCAGAGTGCACCGAGGTGCTACAAGCTATTTGCCAAGATAA	1969
Db	1551	TGCCGGCCTCCAAAGTCTCACTGGGGCGCCAGCTTTACTGCAAGCCATTTGCCAAGGATAA	1610
Qy	1970	CATCATACCTTCTTGAGGGTTTTGGCCACAGCAAGCAATGGGAACTTACCTGGGC	2029
Db	1611	CATCATCCCTTCTCCGGGTGTTTGGCCACGGGAAGCAATGGTGAGCAACGTGGGC	1670
Qy	2030	TTTACTTCTAATGCTGCCATTTGCAGAGCTTGGAACTCATTTGCCCTCCCTGGATCTGT	2089
Db	1671	CCTCTCTCTGACAGGCTCATCGCTGAGCTGGGCATCTCATCGCCTCCCTTGACATGCT	1730
Qy	2090	GGCCCCAATCTTTCCATGTTTTTCTCATGTGTTTACCTCTTTGTAACCTGGCATGTGC	2149
Db	1731	GGCCCCCATTTCTCCATGTTCTTCTGATGTGTTTACCTCTTTGTAACCTGGCCTGTGC	1790
Qy	2150	CTTGTCAACATTACTTTCGAACACCACTGGAGACCCCGATTCGGCTACTACCATTTGGC	2209
Db	1791	TGTGCAGACATTTCTGAGGACCCCACTTGGGGCCCCGGTTCAGATCATCATCTGGGC	1850
Qy	2210	CCTTTCTTTTCATGGGAATCAGTATCTGCTGGCTCTGATGTTTCAATTTCTCTGGTATTA	2269
Db	1851	GTGTGCTTTCTGGGCACTGAGTCTGCTGGCTCTCATGTTGTCTCTCTCTGGTACTA	1910
Qy	2270	TGCCATTGTAGCCATGGTAATAGCTGGTATGATCTACAAGTACATTTGAATACAGAGAGC	2329
Db	1911	CGCCCTTAGTGGCCATGGTCATCGCAGGCATGATCTACAAGTACATCGATACCAAGGGC	1970
Qy	2330	TGAGAAAGATGGGGTATGTTATCCGTGGCTGCTCCCTCAGTGCAGCCCGGTTGCTTT	2389
Db	1971	TGAGAAAGATGGGGTATGTTATCCGTGGCTGCTCCCTCAGTGCAGCCCGGTTGCTTT	2030
Qy	2390	GCTTCGATTGGAGGAAGGACCTCCACACATAAAAACTGGAGCCCTCAGTGTGTTGTAAT	2449
Db	2031	GCTGAGACTAGAGGAAGGCTCTCTCACAGGAACCTGGCGCCTCAGCTCCTGGTCT	2090
Qy	2450	ACTGAACCTTAGATGAAGACTTACATGTCAAGCATCTCTCGCTCTCCTCAGCTCAGCA	2509
Db	2091	GCTGAAGTGTAGAGGAAGATCTTCAATGTGAAGTACCTCGGCTCCTCACCTTTGCTCCA	2150
Qy	2510	GCTCAAGCAGGAAAAAGTNTCACTATTGTGGGCTCTGTCATCTGTGGGAACTTCTCTAGA	2569
Db	2151	ACTTAAGGCTGGGAAAGGCTTGACAAATCGTTGGCTCTGTCATCCAGGCGAGCTTCTGGA	2210
Qy	2570	GAACTACGGTGAAGCTTTAGCTGTGACGACACATTAAGCACCTTAATGGAGGACAGAAA	2629
Db	2211	GAGCTATGGGGAAGCCAGGCTGTGTGAGCAGACAATCAAGAACATGATGGAGATTGGAAA	2270
Qy	2630	GGTAAAGGATTTCTGCCAGCTGTGTGGCGCCCAAGCTGAGAGAGGCAATTTCCCACT	2689
Db	2271	AGTAAAGGCTTCTGCCAGGTAGTGTGGCCAGCAAGGTTGAGAGGGGCTGGCCCACT	2330
Qy	2690	CATCCAGTCACTGTGGCCTTGGGGCATGAAGACAACAACCGGTGTGTATGGGTGGCCCTAA	2749
Db	2331	CATCCAGTCTTGGCGCTGGGTGGCATGAGACATAAATCCCGTGTGTGGGTGGCCCTA	2390
Qy	2750	TGGTGGCGTCAAAAGCGAAGATGCCCGCTTTGGAAGACTTTTATTTGGCACAGATTCGAGT	2809
Db	2391	TGGTGGCGACAGAGTGAAGACCCACGCTGCTGGAAGACCTTTATTCGACACTGTGCGCTG	2450
Qy	2810	GACAACTGCTGCCCATCTTGCACCTGCTGGCTGCTAAACACATCTCTTCTTCCAGCAA	2869
Db	2451	CACCACAGCTGCCCACTGGCCCTGCTGGTGGCAAGAACATAGCTTTCTACCCAGCAA	2510
Qy	2870	TGTGAGCAATTTCTGAGGGCAACATTTGATGTGTGTGGATTGTGCAATGATGGGGGAT	2929
Db	2511	CCACGAGGCTACCTGGAGGGCCACATTTGATGTGTGTGGATCGTGCATGACGAGGCAT	2570
Qy	2930	GCTTATGCTACTACATTTCTTACTTAAACAGACAAAGGTGTGGGAAAGTGCAGCATACG	2989
Db	2571	GCTGATGCTGCTGCTTCTCTGCTGGCCAGCATAAGGTTTGGAAAGAGTGGCGATGCG	2630
Qy	2990	GATCTTCACTAGCCCAATTTAGAAGCAACAGTATCCAAATGGAAGAGGACCTAGCCAC	3049
Db	2631	CATTTTACCCTGGCCAGATGGACGACAACAGCATCCAGATGGAAGAGGATCTGGCCAT	2690
Qy	3050	CTTCCATATCATTTACGCATTTGAGCGGAGGTGAGAGTGTGGAGATGCAATGACATGA	3109
Db	2691	CTTCTGTATCACCTCCGCTGGAAGCTGGAAGTGGAGTGGTGTAGATGCAACAGTGA	2750
Qy	3110	TATATCAGCATATCTTACGAGCGCATTTTATGATGAGAAACAAAGTCCCAGATGCTTGC	3169
Db	2751	CATCTCGGCTTACACCTACGAGCGGACACTGATGATGGAGCGCGGTCTCAAAATCTGCG	2810
Qy	3170	GCATATCGGCTATCCAAAACAGAGCGAGACAGAGGACAAATTTGGTGAAGAGCCGAAA	3229
Db	2811	ACAGATGAGGCTTGACCAAAACAGAGCGGGATCGAGAGGCCCAAGCTGGTGAAGGACGGA	2870
Qy	3230	CTCAATGCTACGATTTGACAGCATTTGGCTCTGATGAGGACGAAGACAGAAACCTATCA	3289
Db	2871	CTCGGCTCTGAGGCTTAGAGAGCTCTACTCCGACGAGGAGGATGAGTCTGTACAGGCGC	2930
Qy	3290	GGAGAGGTGCATGACTTGGACAAAAGACAAAGTACATGTCATCCCGGGGACAAAAGC	3349
Db	2931	TGACAAGATCCAGATGACATGACGACAGAGACAAAGTACATGCTGAACCTCTGGGACCCAG	2990
Qy	3350	GAAGTCAATGNAAGATTTCCAGGACCTGCTTAAATGCTGCGGACCAAGTCCAATGTGAG	3409
Db	2991	CCATGCCCTGACAACTTCCGGGAGCTGGTGACATTAAGCGGACCAAGTCCAATGTGCG	3050
Qy	3410	GGGATGCATACAGCAGTGAAACTCAACGAGGTTATAGTTAAACAAGTCCCATTGAAGCAAA	3469
Db	3051	GGGTATGACACTGCTGTGGAAGCTCAATGAAGTCAATGTACACGCTCCCATGTGCCCG	3110
Qy	3470	GCTGTGTTTATTTGAATATGCCAGGCGCACCCCGGAAACCTCAGGCTGATGAATACTACAT	3529
Db	3111	CTGTGCTCTACTGAACATGCCCGGCCCTTAAGAACAGTGAAGGCTGATGAACTACAT	3170
Qy	3530	GGAGTTCCTAGAGTGTCTTACGAGGGACTAGAGCGAGTCTTACTTGTCCGGGGTGGTGG	3589
Db	3171	GGAAATCTTGAAGTCTTAACCGAGGGCTTGAACGGGTGTTGTTGGTGGTGGTGGTGG	3230

```
QY 3590 CAGTGAAGTGATCACCATTATTTCATAACC 3619
Db 3231 CCGGGAAGTCATCACCATTATTTCITGAGC 3260

RESULT 8
ACA56531
ID ACA56531 standard; cDNA; 3722 BP.
XX ACA56531;
AC 06-JUN-2003 (first entry)
DT 06-JUN-2003 (first entry)
DE Human signalling pathway polynucleotide probe SEQ ID NO 1129.
KW Human; probe; ss; array element; Parkinson's disease;
KW signalling pathway population; cancer; adenocarcinoma; leukaemia;
KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
OS Homo sapiens.
XX US6500938-B1.
PN 31-DEC-2002.
XX 30-JAN-1998; 98US-0016434.
PF 30-JAN-1998; 98US-0016434.
PR 30-JAN-1998; 98US-0016434.
XX (INCV-) INCYTE GENOMICS INC.
PA Au-Young J, Seilhamer JJ;
PI WPI; 2003-352189/33.
DR Combination of polynucleotide probes, useful as array elements in a
PT microarray for monitoring the expression of a number of target
PT polynucleotides -
XX Claim 1; SEQ ID NO 1129; 65pp; English.
XX The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1490
CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signaling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=06500938B1.
XX
SQ Sequence 3722 BP; 712 A; 1088 C; 1126 G; 796 T; 0 other;

Query Match 38.7%; Score 1648.4; DB 25; Length 3722;
Best Local Similarity 71.1%; Pred. No. 0;
Matches 2196; Conservative 0; Mismatches 886; Indels 6; Gaps 1;

QY 536 AGGAGATCAATATTTTGTATATAAAATTTGGCACTCTTTGAGGAGNAATGGACACGACC 595
Db 226 AGGAATTGACTACTATGACAGAACTGGCACTGTTTGGAGAAAGACTGGGACATCCGCC 285
```

1670 ATCAACAGATCTGAGATCTGAAGATCTCAGAGTCTATTCGATTTGTTACTATCCT 1729
1366 CTCAAAACCGCTCTGGGGACCTTTCGTGACGCCAGAAAGTCTATCCCTGTGGGACCACTTCT 1425
1730 TGGCATCTGACCACTCTCTTTGTTTATTTAAGCAATGTTGCTCTTTTGGTGCAATGAT 1789
1426 GGCCCATCATTAACATTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1485
1790 TGAAGGGGTGTTCTCAGAGACAAGTTCCGTGATGCTGTGAAGAGTAAATTTGGTGGTAGG 1849
1486 TGAGGGGTGGTCTTCGCGGACAAGTATGCGCATGGTGTACAGAGAACTTGGTGGTGG 1545
1850 CACCTTATCTGGCCATCCCCATGGGTGATTTGTTATGCTCTCTCTTTTCAACATGTGG 1909
1546 CACACTGGCTGGCTTCACTCTGGGTCTGCTGCTGCTGCTGCTCTCTTTTCAACGTGG 1605
1910 GGTGGAATCTAGAGCTCAGAGCTCAGAGTGCACGAGGCTGCTACAGCTATTTGCCAAGATAA 1969
1606 CGCTGGCTCCAGAGCTCAGAGGGGACACGCGCTATTTGCAAGGCCATTTGCCAAGGACAA 1665
1970 CATCATACCGTTCTGAGGGTTTTGGCCACAGCAAGCAATGGGAACTTACCTGGGC 2029
1666 CATCATCCCTCTCTCGGGGTGTTGGCCACGCGAAGTGAATGTGAACCACTGGGC 1725
2030 TTTACTTTAACTGCTGCAATTCAGAGCTTGGAACTCATTTGCTCTCCCTGGATCTTGT 2089
1726 ACTCTCTCTGACGGCACTCATCGCGAGCTGGGCATCTCATCGCTCTCTCGCATGCT 1785
2090 GGGCCCAATTTCTCATGTTTTTCTCATGTGTTTACCTCTTTGTAACCTTGGCATGTGC 2149
1786 GGGCCCAATTTCTCATGTTTTTCTCATGTGTTTACCTCTTTGTAACCTTGGCATGTGC 1845
2150 CTTGCAAAATTTCTGAAACACCACTGGAGACCCGATTCGGTCTACCTACCTATGGGC 2209
1846 GGTGCAAGACTCTCAGAGACCCCACTGGGCGCCCGGTTCAAGTACTATCATCTGGGC 1905
2210 CTTCTTTTCACTGGGAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2269
1906 GCTGCTCTCTCTGGGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1965
2270 TGGCATTTAGCATGTTAATAGCTGGTATGATCTCAAGTATCATTTGAATACCAAGGAGC 2329
1966 TGGCTCTGTTGGGCACTGCTCATCGCGGCGATGATCTACAAATACATCGAGTACCAAGGGC 2025
2330 TGAGAAAGAAATGGGTGATGTTATCGTGGGCTGCTCCTCAGTCAGCGCCGTTGCTTTT 2389
2026 TGAGAAAGAGTGGGTGACGGGATCCAGGCTGCTCCTCAGGCTGCTCCCGCTACGCGCT 2085
2390 GCTTCGATTTGGAGGAGGACCTCCACACACTAAATACTGGAGGCTCAGTTGCTGTTATT 2449
2086 GTTGGCTGGAGGAGGGCTCTCTCACACCAAGAACTGGCGGCGCAGCTGCTGCTGCT 2145
2450 ACTGAAACTAGATGAAGACTTACATGTCAGGATCTCCTGCTGCTGCTGCTGCTGCTGCT 2509
2146 GCTGAAAGCTGGAGGAGGCTTCCAGCTGAAGTACCGCGGCTCTCCTCAGCTTGGCTCCA 2205
2510 GCTCAAGCAGGAAAGGTTTCACTATTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2569
2206 GCTCAAGGCTGGCAAGGCTGACCAATTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2265
2570 GAACTACGTTAGCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2629
2266 GAGCTATGGCGAGGCTCAGCGCGCGAGCAGACCATCAAGAACTGATGAAATTTAGAA 2325
2630 GGTAAAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2689
2326 GGTGAAAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2385
2690 CATCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2749
2386 CATCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2445
2750 TGGCTGGCTGCAAGCGAAGATGCGCGCTTGGAGACTTTTATTTGGCACAGTTCGAGT 2809

2446 CGGCTGGCGACAGAGCGAGGACCCCGCTGCTGGAAGACCTTTCATTTGACACCGTGGCTG 2505
2810 GACAACTGCTGCCATCTTGCACATGCTGGTGGCTTAAATAAATCTCTCTTTTCCAGCAA 2869
2506 CACTAGCGCTGCCACCTTGGCCCTGCTGCTGCCCAAGAACTGCGCTTCTTACCCAGCAA 2565
2870 TGTGAGCAATTTTCTGAGGGCAACATTTGATGCTGTGGTGGATTTGTCATGATGGGGAT 2929
2566 CCAGAGCGCTACCTGGAGGGCCACATAGACGTTGTTGGATCGTGCACGATGGTGGCAT 2625
2930 GCTTATGCTACTACATTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2989
2626 GCTCATGCTTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2685
2990 GATCTTACACTAGTACCCCAATTTAGAGCAACAGATATCCAAATGAAGAGGACCTAGCCAC 3049
2686 CATCTTCACTGCTGGCCAGATGGATGACAAAGCATCCAGATGAAGAGGACCTGGCTGT 2745
3050 CTTCTATATCACTTACGCTTGGAGCGGAGGTAGAGTGGTGGAGATGTCATGACAGTGA 3109
2746 CTTTCTGTACCATCTGCGCTTGGAGCGAGGTGGAGTGGAGATGTCATAACAGTGA 2805
3110 TATATCAGCATATCTTACGAGCGCATTTTGTATGATGGAACAAAGGTCCAGATGCTTCTG 3169
2806 CATCTCTGCATACACTTACGAGCGGACGCTGATGATGAGCAGCGGTGCGAGATGCTGCG 2865
3170 GCATATCGGCTATCCAAACAGAGCGAGACAGAGAGGACAAATTTGGTGAAGACCGAAA 3229
2866 GCAGATGAGACTGACCAAGACTGAGCGGGAGCGAGAACCCAGCTGGTCAAGGATCGGCA 2925
3230 CTCAATGCTACGATTTGACGATTTGCTGATGAGGACGAGACGAGAAACCTATCA 3289
2926 CTGGCCCTGGCTGGAGGCTGCTACTCGACGAGGAAGATGATCTGCACTGGGGC 2985
3290 GGAGAGGTGCATGATGCTTGGCAAAAGACAAAGTATGATGCTCCCGGGACAAAAGC 3349
2986 TGACAAGATCCAGATGACGTGGAACAGGGAACAAAGTACATGACTGAGACCTTGGGACCCAG 3045
3350 GAAGTCAATGAAGGATTCAGGACCTGCTTAAATGCTGCGGACCAAGTCCCAATGTGAG 3409
3046 CCATGCCCTGACAAATTTCCGGAGCTGGTGCACTTAAGCCGGACCAATCCAAATGTGCG 3105
3410 GCGGATGCATACAGCAGTGAACCTCAACGAGGTTATAGTTAAACAGTCCCATGAAGCAA 3469
3106 GCGCATGCACACTGCTGTGAAGCTCAATGAAGTCAATGCTCAGCGCTCCCAAGACCCG 3165
3470 GCTGTTTTTATGTAATATGCGAGGCGCACCCCGGAAACCCCTGAGGATGATGAAGTACAT 3529
3166 CTTGTTTCTCTTAAACATGCTGCGCCACCCAGGAAACAGTGGGCGGACGAGAACTACAT 3225
3530 GGAGTTCTAGAGGTGCTTACCGAGGACTAGAGGAGTCTCTTCTTCTGCGGGGTGGTGG 3589
3226 GGAGTTCTCAGAGGTGCTGACCGAGGCTTGAAGGCTGCTGTTGGTGGCGGTGGTGG 3285
3590 CAGTGAAGTGTACCACTTTTATTCATAACC 3619
3286 CCGTGAAGTGTACCACTTCTCTGAGC 3315

RESULT 9

ABK83499

ID ABK83499 standard; cDNA; 3768 BP.

XX ABK83499;

AC ABK83499;

XX 14-AUG-2002 (first entry)

XX Human cDNA differentially expressed in granulocytic cells #70.

XX Human; ss; granulocytic cell; DNA chip; bacterial infection;

XX viral infection; parasitic infection; protozoal infection;

XX fungal infection; sterile inflammatory disease; psoriasis;

XX

KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX Homo sapiens.
XX WO200228999-A2.
XX 11-APR-2002.
XX 03-OCT-2001; 2001WO-US30821.
XX 03-OCT-2000; 2000US-237189P.
XX (GENE-) GENE LOGIC INC.
XX Beazer-Barclay Y, Weisman SM, Yamaga S, Vockley J;
XX WPI; 2002-435328/46.
XX
XX Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -
XX
XX Claim 1; SEQ ID No 70; 114pp; English.
XX
XX The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis, renal
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 3768 BP; 711 A; 1099 G; 827 T; 0 other;
XX
XX Query Match 37.2%; Score 1584; DB 24; Length 3768;
XX Best Local Similarity 70.7%; Pred. No. 0;
XX Matches 2122; Conservative 0; Mismatches 872; Indels 6; Gaps 1;
XX
XX 536 AGGAGATGAATATTTTGATAAAATTTGGCACTCTTTGAGGAAGAAATGGACACGACC 595

Db 171 AGGAATTGACTACTATGACAGAAACCTGGCACTGTTTGAGGAAGAGCTGGACATCCGCC 230
Qy 596 GAAGGTGTCTTCCCTCTCAACCCGATGGCCAAATTTACACTAATCTGACTCAAGGAGCAAA 655
Db 231 AAAGTATCGTCTCTCTGGGAAAGCTCGTACGTACACCAACCTCACCAGGGGCCAA 290
Qy 656 GGAACATGAAGAGGAGAAACATCATCTGAAGGAAAGAAAGAGCCCAACAGACCCCA 715
Db 291 AGAGCATGAGGAGCCGAGAGTGGGGGAGCCCGCGGAGGGGAGCCGAGGACCCAG 350
Qy 716 AATGGTACCTTTCATGGGTGTCTACCTCCCATGCTACAAATATTTTGGAGTGATCCT 775
Db 351 CATGGGACCTCTCATGGGGTGTACCTGCCCTGCTGCAGAAATATCTTTGGGTTATCCT 410
Qy 776 TTTTTCACGCTTACATGGGTGTGGGCACAGCTGGAGTCTTTCAGGCTTTTGAATGT 835
Db 411 CTTCCTGGGCTGACCTGGATGGTGGGCACAGAGGTGTCTACAGGCCCTCTCATCGT 470
Qy 836 CTTTATCTGCTGCTGTGTACAAATGTTGACTGTCTATCTTCATGAGTGCATGGCACTAA 895
Db 471 GCTTATCTGCTGCTGTGTGTACCTGCTGACGCCCATCTCCATGAGTGCATCGCCACAA 530
Qy 896 TGGAGTGTGCGCAGCTGGGGCTCATCTTTATGATTTCCGGGACATGGGCCAGAGTT 955
Db 531 CGGTGTGGTCCAGCTGGGGCTCTATTTTCATGATCTCTGTCACCTGGGGCCAGAAAT 590
Qy 956 TGGTGGGGCTGTTGGCCCTCTGCTTTTATCTTGGTACCACATTTGCGAGCAGCATGTACAT 1015
Db 591 TGGAGGTGCTGTGGGCTCTGCTTCTACCTGGGAACAACATTCGAGCAGCGCATGTACAT 650
Qy 1016 CTTTGGTGGCAATGAATTTCTTGTGTATATCGTCCCCGAGCTGCCATCTTTACAG 1075
Db 651 CTTGGGGCCATCGAGATCTGTGACTACATATGCCCCACAGCTGCCATTTTACCC 710
Qy 1076 TGATGAGCACTCAAGAAATCAGCAGCATGCTAAATAACATGCTGTCTAGGCACAGC 1135
Db 711 ATCGGGTCTCATGACACGTCGAATGCCACTTTTGAACAATATGCTGTGTATGGACCAT 770
Qy 1136 TTTCTTGGTCTTATGATGATTTAGTGGTATTTATCGGCTACGCTATGTGAACAAGTTTGC 1195
Db 771 TTTCTGACCTTCATGACCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 830
Qy 1196 CTCANTTTTCTGCTGCTGTGTGATTTGTTCATCTTGGCCATCTATGCTGGAGCCATCAA 1255
Db 831 CTGCTCTTCTGCTGCTGTGTGATCATCTCCATCTCTCCATCTATGCTGGGGCATAAA 890
Qy 1256 GTCTTCTTTTGTCTCTCCACATTTCCGGTGTGCTGCTGGGTAAACCGCATCTTTTATC 1315
Db 891 GTCTATATTTGACCTCTCCGCTGTTTCCGGTATGCTGTGGGCAACAGGACCTGTCCCG 950
Qy 1316 AAGACACATTGACGTTTGTCTTAAGACCAAGAAATTTAAACAACATGACAGTCCCATCAA 1375
Db 951 GGACCATTTGACATCTGTGCCAAGACAGCTGTAGTGGAACATGAGACAGTGGCCACCA 1010
Qy 1376 GTTATGGGATTTCTTGTAACTGAGTCAATTTTCAATGCCACCTGTGATGAATACTT 1435
Db 1011 GCTATGAGTTTCTTCTGCGACAGCCCCAACCTTTACACGACTCTCTGTGACCCCTACTT 1070
Qy 1436 TGTTCACAAATACGTCACTTCAATCCAGGCAATCTCTGGATTTGGCTAGTGTATTAATAC 1495
Db 1071 CATGCTCAACAATGTGACCGAGATCTCTGGCATCCCCGGGGCAGCTGTGTGTGTCTCA 1130
Qy 1496 AGAAGATTTTGGAGTAATTTACCTTACCAGGGAGAGATCATCCAAAGCCCTTCAGCAA 1555
Db 1131 GGAAGACCTGTGGAGCCCTTACCTTGGAGAGGGTGAATCTGTGGAGAGCATGGGTGCC 1190
Qy 1556 ATCTTCTGATGTCTTAGGCAGCTTTAAA-----CCATGAATATGTTCTTGTGTGACATCAC 1609
Db 1191 CTCGAGATGCCCGAGCCTGAAGGAGAGCCTCTGTACGTGTGTGCTGACATCGC 1250
Qy 1610 CACTCTCTCAGCGTCTCTGTGGGAATCTTCTTTTCCCTCTGTTTACAGTATCATGTGTGG 1669

Db 1251 CACATCTTACCGTCTGGTCCGCATCTTCTTCCCTTCTGTAACAGGCATCATGGCTGG 1310
Qy 1670 ATCAACAGATCTGAGATCTCAAGATGCTCAGAACTCTATTCGATGGTACTATCCT 1729
Db 1311 CTCAAACCGCTCTGGGACCTTCGTGACGCCCAAGATCTATCCCTGTGGGACCATCTCT 1370
Qy 1730 TGCCATCTGACCACTCTCTTTGTTTATTAAGCAATGTGTCCTTTTGGTGCAATGAT 1789
Db 1371 GGCCATCATTAACAATCTCTCTGTTACTTACGAGTGTGGTCTCTTTGGTGCTGCAT 1430
Qy 1790 TGAAGGGTGTCTTCAGAGACAAGTTCCGTGATGCTGTGAAGGTAATTTGGTGATGG 1849
Db 1431 TGAGGGTGTGGTCTCCGGGACAAGTATGGCGATGGTGTTCAGCAGGAATCTGGTGTTGG 1490
Qy 1850 CACCTTATCTGGCCATCCCATGGGTGATGTTATTTGGCTCTCTTTTCAACATGGG 1909
Db 1491 CACACTGGCTGGCTTCACTTGGGTCTATGTCATCGGCTCTCTTTTCAACGTGG 1550
Qy 1910 GGCTGGACTTCAGAGCTCACAGGTGCACCGAGGCTGCTACAAGCTATTGCCAAGGATAA 1969
Db 1551 CGCTGGCTCCAGAGCTCACAGGGGCACACGCTATTGCAAGGCAATGCCAAGGACAA 1610
Qy 1970 CATCATACCGTTCTGAGGGTTTTGGCCACAGCAAGCAATGGGAACTTACCTGGGC 2029
Db 1611 CATCATCCCTCTCTCCGGGTGTTTGGCCACGGGAAGGTGAATGTGTGAACCCACATGGGC 1670
Qy 2030 TTTACTTCTAACTGCTGCTGCATTTGCAGAGCTTGAATACTCATTTGCTCCCTCGATCTGT 2089
Db 1671 ACTCTCTGACGGCACTCATCGCGAGCTGGGCATCTCATCGCTCTCTCGCATGGT 1730
Qy 2090 GGCCCCAATTTCTTCCATGTTTTTCTCATGTGTTTACCTCTTTGTAACCTTGGCATGTGC 2149
Db 1731 GGCCCCCATCTTATCCATGTTCTTCTGATGTGCTACCTGTTCTGTAACCTCGCTGTGC 1790
Qy 2150 CTTGCAAAATTAATTCGAACACCCAACTGGAGACCCCGAATTCGGCTACTACATTTGGGC 2209
Db 1791 GGTGACAGACTCTGAGGACCCCAACTGGGGCCCGGTTCAAGTACTATCACTGGGC 1850
Qy 2210 CTTTCTCTTCATGGGAATGATATCTGCTGGCTCTGATGTTTCTTCTCTGTTATTA 2269
Db 1851 GCTGTCTCTCTGGGCATGAGTCTGCTGGCCCTTATGTTGTCTCTCTCTGGTACTA 1910
Qy 2270 TGCCATTTAGCCATGGTAATAGCTGGTATGATCTACAAGTACATTAATACCAAGGAGC 2329
Db 1911 TGCCCTGTGGCATCTCATCGCGCATGATCTACAAATATACATGAGTACCAAGGGGC 1970
Qy 2330 TGAGAAAGAAATGGGTGTATGTTATCCGTGGGTGTCCCTCAGTGAGCCCGGTTTGTCTTT 2389
Db 1971 TGAGAAAGGATGGGGTGAAGGGATCCGAGGCTGTCCCTGAGCGCTGCCCGCTTACGCGCT 2030
Qy 2390 GCTTCGATTTGGAGGAAGGACCTCCACACATAAATCGAGGCTCAGTTGCTGTATT 2449
Db 2031 GTTGGCGCTGGAGGAGGGGCTCTCACACCAAGAACTGGCGGCGCAGCTGCTGGTGTCT 2090
Qy 2450 ACTGAAATAGATGAAGACTTACATGTCAAGCATCTCGCTCTCTCACTCTTGGCTCACA 2509
Db 2091 GCTGAAGCTGGACAGGACCTTCACTGAAGTACCCGCGCTCTCACTCTCGCTCCCA 2150
Qy 2510 GCTCAAAGCAGGAAAGGTTNCTACTATTTGGGCTCTGTATGTTGGGAACTTCCCTAGA 2569
Db 2151 GCTCAAGGCTGGCAAGGGCTGACCATTTGTTGTTCTGTATCCAGGGAGGCTTCTTGA 2210
Qy 2570 GAACTACGGTGAAGCTTTAGCTCTGAGCAGACCATTAAGCACCTAATGAGGCGACAGAA 2629
Db 2211 GAGCTATGGCGAGGCTCAGGCCCGGAGCAGACCATCAAGAAATGATGAATTTAGAA 2270
Qy 2630 GGTAAAGGATTTGTCAGCTGTGTGGTGGCCGCAAGCTCAGAGAGGCAATTTCCCACT 2689
Db 2271 GGTGAAGGGCTTCTGCCAGTGTGTGTGGCCACCAAGGTGGGAGGGGTGCGCCACCT 2330
Qy 2690 CATCCAGTATGTTGGCTTGGGGGCATGAAGCAACAACAGGTGTGATGGCTTGGCTTAA 2749
Db 2331 CATCCAGTCTGTGGCTTGGGAGGCATGCGGCATAACTCCGTGTGTCTGGGCTGGCCCTA 2390

Qy 2750 TGGTGGCTCAAAAGCGAAGATGCCCGCTTGAAGACTTTTATGSCACAGTTCGAGT 2809
Db 2391 CGGTGGCGACAGAGCGAGGAGCCCGCTGCTGCTGAAGACCTTTCATTGACACCGTGGCTG 2450
Qy 2810 GACAACTGCTGCCCATCTTGCACCTGCTGGTGGCTTAAAAACATCTCTTCTTCCAGCAA 2869
Db 2451 CACTACGGCTGCCCATCTGGCCCTGCTGTCGCCCAAGAACATCGCTTCTTACCCAGCAA 2510
Qy 2870 TGTGAGCAATTTTCTGAGGGCAACATTTGATGTGTGGTGGATTTGTCATGATGGGGGAT 2929
Db 2511 CCACAGCGCTTACCTGAGGGCCACATAGACGTGTGTGGATCTGTGACGATGTGGGAT 2570
Qy 2930 GCTTATGCTACTACCATTTCTTACTGAAACACACAAAGGTGTGGGAAAGTGCAGCATACG 2989
Db 2571 GCTCATGCTTCTGCCCTTCTGCTGCGCCACGATAGGTCTGGAGGAAGTCCGATGCG 2630
Qy 2990 GATCTTCACTAGTACCCCAATTTAGAAGCAACAGTATCCAAATGAAGAAGGACCTTAGCCAC 3049
Db 2631 CATCTTCACTAGTGGCCAGATGATGACACAGCATCCAGATGAAGAAGGACCTTGGCTGT 2690
Qy 3050 CTTCTATATCACTTACGCTTGGCGGAGGTAGAGTGTGGTGGAGATGCATGACAGTGA 3109
Db 2691 CTTTCTGTACCATCTGCGCCTTTGAGGCGAGGTGGAGTGTGGAGATGCAATAACAGTGA 2750
Qy 3110 TATATCAGCATATATCTTACGAGCGCATCTTTGATGATGGAAACAAAGGTCTCCAGATCTTCG 3169
Db 2751 CATCTCTGCATACCTTACGAGCGGACGCTGATGATGGAGCAGCGTCCGAGATGCTGCG 2810
Qy 3170 GCATATGCGGTATTCACAAAACAGAGCGAGACAGAGAGGCAAAATTTGGTGAAGACCGAAA 3229
Db 2811 GCAGATGAGACTGACCAAGACTGAGCGGGAGCGGAGAGCCAGCTGGTCAAGGATCGGCA 2870
Qy 3230 CTCATGCTACGATTTGACAGCATTTGGCTCTGATGAGGACGAGACGAGACAGAAACCTATCA 3289
Db 2871 CTCGCGCTCTGGCTGGAGCGCTGTACTCGGACGAGGAAGATGATCTGACAGTGGGGGC 2930
Qy 3290 GGAGAAGGTGCACATGACTTGGACAAAAGAACAAAGTACATGTCATCCCGGGGACAAAAGC 3349
Db 2931 TGACAAAGATCAGATGACGTGACACAGGACCAAGTACATGACTGAGACCTGGACCCAG 2990
Qy 3350 GAAGTCAATGAAGGATTTCCAGGACCTGCTTAAACATGCGTCCGGACCAAGTCCAATGTGAG 3409
Db 2991 CCATGCCCTCACAATTTCCGGGAGCTGGTGACATTAAGCGGACCAATCCAATGTGCG 3050
Qy 3410 GCGGATGATACAGCAGTGAACCTCAACGAGGTTTATGTTAACAGTCCCATGAAGCAAA 3469
Db 3051 GCGCATGACACTGCTGTGAAGCTCAATGAAGTCAATGTACGCGCTCCCAGACGCCG 3110
Qy 3470 GCTGTTTTTATTTGAATATGCCAGGCGCACCCCGAAACCTCAGGGGTGATGAAAACATCAT 3529
Db 3111 CTTGTTCTCTTAAACATGCTTGGCCACCCAGGACAGTGAAGGCGGACGAGAACTGAT 3170

RESULT 10

AAS59387

ID AAS59387 standard; cDNA; 5239 BP.

XX

AC AAS59387;

XX

DT 16-JAN-2002 (first entry)

XX

DE Human cDNA encoding potassium-chloride cotransporter KCC4.

XX

KW Human; ss; potassium-chloride cotransporter; epilepsy; hypertension;
KCC; hypotensive; anticonvulsant; antianaemic; sickle-cell anaemia;
gene therapy.

XX

OS Homo sapiens.

XX

PN WO200179525-A2.

XX

PD 25-OCT-2001.

XX 16-APR-2001; 2001WO-US12395.
 XX PF
 XX 14-APR-2000; 2000US-197350P.
 XX PR
 XX (UYVA-) UNIV VANDERBILT.
 XX PA
 XX (GAMB/) GAMBA G.
 XX
 XX Gamba G, Mount DB, Delpire E, George AL;
 XX PI
 XX WPI; 2001-611726/70.
 DR P-PSDB; AAU39092.
 DR
 XX
 XX New isolated and purified potassium-chloride cotransporter polypeptide
 PT for detecting a modulator of potassium-chloride cotransporter that can
 PT treat epilepsy, sickle cell anaemia, and hypertension -
 XX
 XX Claim 24; Page 205-213; 352pp; English.
 XX
 XX The invention relates to an isolated and purified, biologically active
 CC KCC2, KCC3, or KCC4 potassium-chloride cotransporter polypeptide
 CC and polynucleotides encoding them. KCC and the nucleic acid encoding KCC
 CC are used to produce an antibody against KCC, which can be used to detect
 CC KCC. The antibody and nucleic acid are used in kits to detect KCC and
 CC the nucleic acid encoding KCC. KCC and nucleic acid encoding it are used
 CC to screen for candidate substances that can modulate the activity of KCC.
 CC KCC and the nucleic acid encoding it can be used to modulate potassium-
 CC chloride cotransport in a vertebrate. Therapeutic compositions
 CC comprising modulators of the activity of KCC (preferably antibodies or
 CC antisense oligonucleotides) are used to treat epilepsy, sickle cell
 CC anaemia, and hypertension (also via gene therapy using the KCC
 CC polynucleotide). The present sequence encodes a KCC of the invention.
 XX
 XX Sequence 5239 BP; 1015 A; 1612 C; 1560 G; 1049 T; 3 other;
 SQ

Query Match 33.3%; Score 1418; DB 22; Length 5239;
 Best Local Similarity 66.9%; Pred. No. 0;
 Matches 2104; Conservative 0; Mismatches 1010; Indels 33; Gaps 5;

QY 483 GACGACATAGAAAGCTCGAAATGCTTATCTCAATAATTCCTCAATGAAAGAGGAT 542
 |||||
 DB 131 GATGAAATCCAAAGAGAAACAGCCCATTCNTCAACATGTCGAGGTGGAACAGAGAGC 190
 |||||
 QY 543 GAATATTTTGATAAAAATTTGGCACTCTTTGAGGAAGAAATGGACACAGACCGAAGGTG 602
 |||||
 DB 191 TTCTTTGAAGGGAAGAACATGGCACTTTTCGAGGAGAGATGGACAGTAACCCCATGGTG 250
 |||||
 QY 603 TCTTCCCTCCCAACCGATGSCCAATTACACTATCTGACTCAAGGAGCAAGAAACAT 662
 |||||
 DB 251 TCCTCGCTGNTCAACAGCTGGCCCACTACACCAACCTGAGCCAGGGCGTGGTGAGCAC 310
 |||||
 QY 663 GAAGAGGAGAAACATCACTGAAGGGGAAAGAGCCCAACAGACCCCCCAATGGGT 722
 |||||
 DB 311 GAGGAGGAGGAGAGCGCGGGGGGA-----GGCAAGGCTCCGGCATGGGC 361
 |||||
 QY 723 ACCTTCATGGGTGTACTCTCCCATGTCTACAAATATTTTGGAGTATCTTTTPTTA 782
 |||||
 DB 362 ACCTTCATCGGCGTCTACCTGCGGTGCTGAGAACATCTCTGGGGTCTATCTCTCTG 421
 |||||
 QY 783 CGCCTTACATGGGTGGGACAGCTGGAGTTCTTCAGGCTTTTGGCAATTTGCTCTTATC 842
 |||||
 DB 422 CGCCTGAAGTGGTGGGGGTGGTGGTCTCTGAGTCTCTCTCATCTGGGCCATG 481
 |||||
 QY 843 TGCTGCTGTGTACAAATGTTGACTGTCTATCTCCATGAGTGGCATTTGCCACTAATGGAGTG 902
 |||||
 DB 482 TGCTGCACATGTACAAATGCTGACCGCCATTTCCATGAGTGGCATCTACCAACGGTGTG 541
 |||||
 QY 903 GTGCCAGCTGGGGGTCTACATCTTTATGATTTCCGGGCACTGGGGCCAGAGTTTGGTGGG 962
 |||||
 DB 542 GTCCAGCTGGGGGTCTCTACTACATGATATCGCGCTCGCTGGGACCCGAGTTTGGAGGC 601
 |||||
 QY 963 GCTGTTGGCTCTGCTTTTATCTTGGTACCACATTTTGGCAGGACCATGTACATCTTGGT 1022
 |||||

DB 602 GCTGTGCGCTCTGCTTCTACTGGGACAGAGCTTTTGCAGGGGCATGTATATTTTGGGG 661
 QY 1023 GCCATTGAAATCTTTTCTGGTCTATATCGTCCCGAGCTGCCATCTTTTCACAGTATGAC 1082
 |||||
 DB 662 ACCATCGAGATTTTCTGACGTACATCTCCCGGTGGGCCATCTTCCAGGCGAGGCT 721
 |||||
 QY 1083 GCACCTCAAGGAATCAGCAGCCATGCTAAATAACATGCGTGTCTACGGCAGCAGCTTTCTTG 1142
 |||||
 DB 722 GCAGGTGGCGAGGCGGCCCATGTCACAAACATGCGTGTGTACGGCAGCGTCAACGCTC 781
 |||||
 QY 1143 GTCCCTATGTTAGTGGTATTTTATCGGCGTACGCTATGTGAACAAGTTTGCCTCANNT 1202
 |||||
 DB 782 GTGCTATGCGCCCTGGTGGTCTTCTGTTGGCGCTCAAGTATGTCAACACTGGCGCTGTC 841
 |||||
 QY 1203 TTCTGCGCTGTGTCAATTTGTCTCATCTTGGCCATCTATGCTGGAGCCATCAAGTCTTCT 1262
 |||||
 DB 842 TTCTGCGCTCGTGTGCTGCTCATCTGCGCCATCTATGCGCGCTCATCAAGTCTGCC 901
 |||||
 QY 1263 TTTGCTCTCCACACTTCCCGGTCTGCATGCTGGGTAACCGCACTCTTTTCATCAAGACAC 1322
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 DB 902 TTCGACCCCGGACATCCCGGTCTGCTCTGCGGAAACCGCACGCTGTCAAGCGCGAGC 961
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 QY 1323 ATTGACGTTTGTCTCTAAGACCAAGGAAATTAACAACATGACAGTCCCATCAAGTTATGG 1382
 |||||
 DB 962 TTCGATGCTGCTCAAGGCTTACGGCATCCACAACTCAAGCCACCTCCGCGCTCTGG 1021
 |||||
 QY 1383 GGATTTCTGTAACTCGAGTCAATTTTTCATGCCACCTGTGATGAATACTTTGTTTCCAC 1442
 |||||
 DB 1022 GGCCTCTTCTGCAACGGCTCCCA--GCCAGCGCGGCTGTGACGAGTACTTTCATCCAG 1078
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 QY 1443 AATAAGCTCACTTCAATCCAGGGCATCTCTGGATTGGTGTAGTGTATTAATTACAGAGAT 1502
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 DB 1079 AACAACTCACCAGAAATCCAGGGCATCCCGGCGCGGCTGTGTTCTTCTTGAGAAC 1138
 |||||
 QY 1503 CTTTGGAGTAAATTACCTACCAAGGGAGAGATCATCGAARA-----GCCTTCAGCC 1553
 |||||
 DB 1139 CTGTGGAGTACGTACGGCACCGGGGGCGTTTGTGGAGAAAGGTGTGCCCTCGGTG 1198
 |||||
 QY 1554 AAATCTTCTGATGTCTTAGGCAGCTTAAACCATGAATATGTTTGTGTGACATCACCAACC 1613
 |||||
 DB 1199 CCGGTGCGAGAGAGAGCGGTGCCAGCACACTGCCCTACGTGCTCACCGCATCGCGGCC 1258
 |||||
 QY 1614 TCCTTCAAGCTCTGGTGGGAATCTTCTTCCCTCTGTGTTACAGGTATCATGGCTGGATCA 1673
 |||||
 DB 1259 TCCTTCAAGCTCTGGTGGCATCTACTTCCCTTCCGTGACCGGTATCATCGCGGTTC 1318
 |||||
 QY 1674 AACAGATCTGAGATCTGAAGATGCTCAGAGTCTATTCGATTTGTTGTTTCTTCTTCC 1733
 |||||
 DB 1319 AACCGTCCGGGAGACCTCAAGGATGCACAGAGTCCATCCCCACGGGACCATCTCTGGCC 1378
 |||||
 QY 1734 ATCTGACCACTCTCTTTGTTTATTTAAGCAATGTTGTCCTTTTGTGTCATGTATTGAA 1793
 |||||
 DB 1379 ATAGTGACGAGCTCTTCACTATCTCTCTGTCATGCTGTGTTTGGGCGCTGCATTGAA 1438
 |||||
 QY 1794 GGGTGTGTTCTCAGAGACAAAGTTCCGTGATGCTGTGAAGGTAAATTTGGTGGTAGGCACC 1853
 |||||
 DB 1439 GCGTGTGTTCTTACAGATAAGTTCCGGGAGGCCCTGTCAGGGGAACCTGGTTCATCGGCATG 1498
 |||||
 QY 1854 TTATCTTGGCCATCCCATGGTGTATTTTATTTGGCTCTTCTTTTCAACATGTGGGCT 1913
 |||||
 DB 1499 CTGGCTTGGGCGCTCCCGCTGGGTCTCATGTCATGGCTCTTCTTCTCCACCTGGGTGCC 1558
 |||||
 QY 1914 GGACTTCAGAGCCCTCAGAGTGACCGAGGCTGTCTACAAGCTATTGGCAAGATAAATC 1973
 |||||
 DB 1559 GGCCTGCAGACCTCAGCGGGGACCGGCTACTGAGGGCCATTTGCCGTGACGGCATC 1618
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 QY 1974 ATACCGTTCTGAGGGTTTTTGGCCACAGCAAGCCAAATGGGAACTTACCTGGGCTTTA 2033
 |||||
 DB 1619 GTCCCTCTCTGAGGTGTTTGGCCAGGGAAAGCCCAACGGGAGCCCACTGGGCGGTG 1678
 |||||
 QY 2034 CTTCTAATGCTGCCATTTGAGAGCTTGGATACTCATTTGGCTCCCTCGGATCTTGTGGCC 2093
 |||||
 DB 1679 CTGCTGACAGTCTCATCTCGGAGACTGGCATCCTCATCGCCTCTCTGGGACAGCTGGCC 1738
 |||||

Qy	2094	CCAAATCTTTCCATGTTTTTTCTCATGTGTTTACCTCTTTGTAAACATTGGCATGTGCTTTG	2153
Db	1739	CCGATCCTCTCCATGTTCTTCCATCATGTCTACCTGTTCTGTGAACCTGGCCTCGCGCGTG	1798
Qy	2154	CAAAACATTACTTCGAAACACCAACTCGAGACCCCGATTCGCGTACTACCAATCGGGCCCTT	2213
Db	1799	CAGACCTGTGTACGTATACCCCAACTGCGGCTCCACGCTTCAAGTCTTACCACTCGACCCCTG	1858
Qy	2214	TCCTTTCATGGGAATGAGTACTGTCCTGCGCTCTGATGTTCAATTTCTTCTCTGTTATATGCC	2273
Db	1859	TCCTTTCCTGGGTATGAGCCTGTGCTCGCGCTGATGTTCAATCTGCTCCTCGTACTACGCG	1918
Qy	2274	ATTGTAGCCCATGGTAATAGTGTGTTATGATCTACAAGTACATCTGAATACCAAGAGAGTGTAG	2333
Db	1919	CTGTCCGCCATGCTCATCGCTGGCTGCATCTACAGTACATCGAGTACCGCGGGCCGAG	1978
Qy	2334	AAAGAAATGGGGTGATGTATCCGTGGGCTGTCTCCTCAGTGAGAGCCCGGTTTGTCTT	2393
Db	1979	AAGGAGTGGGGCGATGGCATCCGTGGGCTATCCCTGAACGCGCGCCCTACGCCCTGCTG	2038
Qy	2394	CGATTGGAGNAGSACCTCCACACACTAAAAACTGGAGGCTCAGTGTCTGTGTTATTAATCTG	2453
Db	2039	CGCGTGAGACAGCGTCCCGCCCAACCAAGAACTGGAGGGCCCAAGTGTCTGTGATGCTG	2098
Qy	2454	AAACTAGATGAAGACTTACATGTCAAGCATCTCTCGCCTCTCACTTTGTCTCACAGCTC	2513
Db	2099	AACTGTGACGGAGAGCGGCGTGAAGCAACCCCGCCTGTCTGTCTTCACTCGTCCGAGCTG	2158
Qy	2514	AAAGCAGGAAAGGTNTCACTATTGTGGGCTGTGTATCGTGGGGAATCTCTTAGAGAAC	2573
Db	2159	AAGCCCGCAAGGCGCTGACCATCGTGGGCTCGGTGTGGAGGGAGCTACCTGGACAAG	2218
Qy	2574	TACGGTGAAGCTTTAGCTGTGACGACACACATAAAGCACCTTAATGGAGGCGAGAGAGGTA	2633
Db	2219	CACATGGAGGCTCAGCGCGGCGGAGGAAACATACCGTCCCTAATGAGCAACAGAGAAGACC	2278
Qy	2634	AAAGGATTTCTCCAGCTGGTGGTGGCGCGCAAGCTGAGAGAGGCAATTTCCCACTCATC	2693
Db	2279	AAGGGCTTCTCGAGCTGGTGGTCTCGTCAAGCCTGCGGATGGCATGTCTCCACCTGATC	2338
Qy	2694	CAGTCATGTGGCCTTTGGGGGCGATGAAGCAACACGTTGTGTGATGGGCTGGCCCTAAATGGC	2753
Db	2339	CAGTCGGCGGCGCTGGGCGGCGCTGAAGCACAAACGTTGCTATGGCCTGGCCCGCATCC	2398
Qy	2754	TGGCGTCNAAGCGGAAGATGCCCGCGCTTGGNAGACTTTATTGGCACAGTTTCGAGTGACA	2813
Db	2399	TGGAAGCAGGAGGACAACCCCTTCTCTCGGAAGAACTTTGTAGACACCGTCCGCGACACC	2458
Qy	2814	ACTGTGCGCCATTTGTCACTGCTGGTGGCTAAAAACATCTCTTCTTTTCCAGCAATGTG	2873
Db	2459	ACCGCGCGCACAGGCTCTGCTGGTGGCCAAAGAAACGTGACTGTTTCGCAAAACACAG	2518
Qy	2874	GAGCAATTTCTGAGGGCAACATTGATGTGTGGATTGTGCAATGATGGGGGATGCTT	2933
Db	2519	GAGCGCTTCGGCGGGGCCACATCGACGTGTGTGGATCGTGCACGACGCGCGCATGCTC	2578
Qy	2934	ATGCTACTACATTCCTACTGAAACAGCACAAAGGTGTGGCGAAATGAGCATACGGATC	2993
Db	2579	ATGCTGTGTGCCCTTCTCTCTCGCCAGCACAAAGGTGTGGAGGAAGTGC CGGATCGGTATC	2638
Qy	2994	TTCCAGTAGCCCAATTAGAAAGACAAACAGTATCCAAATGAAGAAGGACCTAGCCACCTTC	3053
Db	2639	TTACCGTGGCCAGGTGGACGACAAACAGATCCAGATGAAGAAGGACTTCGCAGATGTTCT	2698
Qy	3054	CTATATCACTTACGCAATTGAGCGGAGGTAGAAGTGGTGGAGATGCATGACAGTGATATA	3113
Db	2699	TTGTATCACTTGGCATCAGCGCGAGGTGGAGGTGGTGGAGATGGTTGAAAACGACATA	2758
Qy	3114	TCAGCATATACTTACGACGCGCACTTTGATGATGAAACAAAGGTCGAGATGCTTCGGGAC	3173
Db	2759	TCTGCTTTTCACTACGAGAGACACTAATATGATGGAGCAGAGGTTCGAGATGCTCGAAGCAG	2818

Qy	3174	ATCGGGCTATCCAAAACAGACGACAGACAGAGAGGACCAATTTGGTGAAGAAGCCCAAACTCA	3233
Db	2819	ATGCAGCTGTCTCAAGAACGACGACGAGGACGAGGCGCCAGCTGTATCCACGACGAGAAACACC	2878
Qy	3234	ATGCTACGATTGACCGACGCAATTTGGCTCTGATGAGGACGAGAGACGAGAAACCTATCAGGAG	3293
Db	2879	GC-----GTCCACACCGCGCGGCGCAGCCAGGACCCAAAGCGCGCCTACGCCAGAC	2929
Qy	3294	AAGGTGCACATGACTTGGACAAAAAGACAAGTACATATGGCATCCCGG---GGACAAAAAGCG	3350
Db	2930	AAGGTGCAGATGACCTGGACACGGAAGAGTCTCGCTGAGAAGTACAGGACGACGAGAC	2989
Qy	3351	AAGTCAATGAAGATTCCAGGACCTGCTTTAAATATGCGTCCGACCGAGTCCATATGTGAGG	3410
Db	2990	ACCAGCTATCCCGTTTCAAGACCTCTTCAGCATGAAGCGGACCCAGTCCAAACGTCAAG	3049
Qy	3411	CGGATGCATACAGCAGTGAACCTCAACGAGGTTATAGTTAAAGTCCCATGAAGCAAAAG	3470
Db	3050	CGGATGCACACCGGCTGTGAAGCTCAATGGCGTCTGTCNTCAACAGTCCCAAGGATCGCGAC	3109
Qy	3471	CTGGTTTTATTGAATATGCCAGGCGCACCCGCAAAACCTCAGGGTGATGAAAACTACATG	3530
Db	3110	CTGGTCTCTCAACATGCCAGTCTCTCCAAAAACCGGACGAGGACGAGAACTACATG	3169
Qy	3531	GAGTTCCTAGAGGTGCTTACCGAGGGGACTAGACGAGTCTCTATTGTCCGGGTGTGTGGC	3590
Db	3170	GAGTTTCTTGAAGTCTCTGACCGAGGGGCTGAACAGAGTCTCTCTGTTCAGGGGTGTGGCGC	3229
Qy	3591	AGTGAAGTGATCACCATTATTATCAAA	3617
Db	3230	CGGAGGTGATCACCATTACTCTCTAA	3256
RESULT 11			
AAK51667			
ID	AAK51667 standard; cDNA; 5263 BP.		
XX	AAK51667;		
AC			
XX	06-NOV-2001 (first entry)		
DT	Human polynucleotide SEQ ID NO 212.		
DE	Human; cytokine; cell proliferation; cell differentiation; gene therapy;		
XX	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;		
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;		
KW	nervous system disorder; arthritis; inflammation; ss.		
XX	Homo sapiens.		
OS	WO200157190-A2.		
PN	09-AUG-2001.		
PD	05-FEB-2001; 2001WO-US04098.		
PF	03-FEB-2000; 2000US-0496914.		
XX	27-APR-2000; 2000US-0560875.		
PR	20-JUN-2000; 2000US-0598075.		
PR	19-JUL-2000; 2000US-0620325.		
PR	01-SEP-2000; 2000US-0654936.		
PR	15-SEP-2000; 2000US-0663561.		
PR	20-OCT-2000; 2000US-0693325.		
PR	30-NOV-2000; 2000US-0728422.		
XX	(HYSE-) HYSEQ INC.		
PA	Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;		
XX	Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;		
PI	Xue AJ, Yang Y, Wejhrman T, Goodrich R;		
XX	WPI; 2001-476283/51.		
DR	P-PSDB; AAM78534.		

2274 ATTGTAGCCATGGTAAATAGCTGTATGATCTTACAAAGTACATTTGAATACCAAGAGCTGAG 2333
| | | | |
Db | | | | |
1938 CTGTCCGCCATGCTCATCGCTGGCTCATCTACAGTACATCGATACCGCGGGCCGAG 1997
| | | | |
Qy | | | | |
2334 AAAGAAATGGGGTGATGGTATCCGTGGGCTGTCCCTCAGTGCAGCCGGTTCCTTTGCTT 2393
| | | | |
Db | | | | |
1998 AAGGAGTGGGGCGATGGCATCCGTGGCTTATCCCTGAACGCCGCCGCTACGCCCTGTGTG 2057
| | | | |
Qy | | | | |
2394 CGATTGGAGAGGACCTCCACACACTAAAACTGGAGGCCCTCAGTTGCTGTATTAATCTG 2453
| | | | |
Db | | | | |
2058 CCGCTGGAGACCGTCCCCCCCCACACCAAGAACTGGAGGCCCGAGTGTGTGTGTGTG 2117
| | | | |
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2454 AAACAGATAGTGAAGACTTACATGTCAAGCATCTCGCTCTCCCTCACCTTTTCCCTCACAGCTC 2513
| | | | |
Db | | | | |
2118 AACCTGGACGGGACGAGCCGCTGAAGCACCCCGCTGCTGTCTTACGTTCGACGTG 2177
| | | | |
Qy | | | | |
2514 AAAGCAGGAAAGGTTNCTACTATTGTGGCTCTGTCTATCTGTGGGAACTTCTCTAGAGAAC 2573
| | | | |
Db | | | | |
2178 AAGGCCGGAAGGGCTGACCATCTGTGGCTCGGTCTGGAGGGGACGTACCTGGACAG 2237
| | | | |
Qy | | | | |
2574 TAGCGTGAAGCTTTAGCTGCTGAGCAGACCATTAAGCACCTTAATGGAGGCAGAGAAGTA 2633
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Db | | | | |
2238 CACATGAGGCTCAGCGGCCCGAGGAGAAACATACGCTCCCTTAATGAGCACAGAGAAGCC 2297
| | | | |
Qy | | | | |
2634 AAAGGATTTCTGCCAGCTGTGTGGCGCCCAAGCTGAGAGAGGCAATTTCCACCTCATC 2693
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Db | | | | |
2298 AAGGGCTTCTGCCAGCTGTGTGTCTGTCTCAGCTCGGGATGGCATGTCCCACTGTATC 2357
| | | | |
Qy | | | | |
2694 CAGTCAATGTGGCTTGGGGGCATGAAGCACACACGCTGTGTGTGTGGCTGTGGCTTAATGCC 2753
| | | | |
Db | | | | |
2358 CAGTCGGCGGCTGGCGGCTGGAAGCACACACGCTGTCTCATGSCCTGGCCGATCC 2417
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Qy | | | | |
2754 TGGCGTCAAGCGAAGATGCCCGCTTGGAGACATTTATTGGGCACAGTTGCGAGTGACA 2813
| | | | |
Db | | | | |
2418 TGAAGCAGGAGGACAAACCTTCTCTGTGAAGAACTTTGTAGACACCGCTCCGCGACAC 2477
| | | | |
Qy | | | | |
2814 ACTGCTGCCATCTTGCATCTGTGGTGGCTTAAACATCTCTCTTTTCCAGCAATGTG 2873
| | | | |
Db | | | | |
2478 ACCGCCGGCAGCAGGCTGTGCTGTGGTGGCCAGACGTCGATCTCTTCGCAAAACAG 2537
| | | | |
Qy | | | | |
2874 GAGCAATTTTCTGAGGGCAACATGTATGTGTGGTGAATGTGCAATGATGGGGATGCTT 2933
| | | | |
Db | | | | |
2538 GAGCGCTTCGGCGGGGCGACATCGACGTGTGTGTGATCTGTGCACGCGCGCATGCTC 2597
| | | | |
Qy | | | | |
2934 ATGCTACTACCTTCTTACTGAACAGCAGCAAGTGTGGCAAGTGCAGCATACGGATC 2993
| | | | |
Db | | | | |
2598 ATGCTGCTGCCCTTCTGCTGCCAGCACAAGTGTGGAGGAAGTGGCGGATGCGGTATC 2657
| | | | |
Qy | | | | |
2994 TTCACAGTAGCCCAATTTAGAAGACAACAGTATATCCAAATGAAGAGGACCTTAGCCACTTC 3053
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Db | | | | |
2658 TTCACGCTGCCAGGTGGACGACACACGATCCAGATGAAGAGGACCTGCAGATGTTTC 2717
| | | | |
Qy | | | | |
3054 CTATATCACTTACGCTTGAAGCGGAGGTAGAGTGTGGAGATGATGATGATGATGATGAT 3113
| | | | |
Db | | | | |
2718 TTGTACCACTTGGCATCAGCGCCGAGGTGGAGTGTGGAGATGTTGAAACACGACATA 2777
| | | | |
Qy | | | | |
3114 TCAGCATATACCTTACAGCGCACTTTGATGATGATGATGATGATGATGATGATGATGATG 3173
| | | | |
Db | | | | |
2778 TCTGCTTTTCACTTACGAGAGGACACTTAATGATGGAGCAGAGGTTCGAGATGCTGTAAGCAG 2837
| | | | |
Qy | | | | |
3174 ATCGCGCTATCCAAAACAGAGCGAGACAGAGGSCACAATTTGGTGAAGAGCCGAAACTCA 3233
| | | | |
Db | | | | |
2838 ATCAGCTGTCCAAAGAACAGAGCAGGAGCGAGGCCCCAGCTGTATCCACGACAGGAACACC 2897
| | | | |
Qy | | | | |
3234 ATGCTACGATTTGACCAAGCATTTGGCTCTGTATGAGGACGAAGAGACAGAAACCTATCAGGAG 3293
| | | | |
Db | | | | |
2898 GC-----GTCCTCACACCGCGCGGCGAGCCAGGACCAAGCGCGCTACGCGCAGAC 2948
| | | | |
Qy | | | | |
3294 AAGTGCAATGATGATGGAACAAAGACAAGTACATGCGATCCCGG---GGACAAAAGCG 3350
| | | | |
Db | | | | |
2949 AAGGTGAGATGACCTGGACCGAGGAGAAAGCTGTATGCTGAGAAAGTACAGGAGCAGAGAC 3008
| | | | |

Qy 3351 AAGTCAATGGAGGATTCCAGGACCTGCTTAAATGCGTCCGGACCACTCAATGTGAGG 3410
| | | | |
Db 3009 ACCAGCCTATCTGGTTTCAAAGACCTCTTACGATGAAGCCGGACCACTCCAAACGTCAGG 3068
| | | | |
Qy 3411 CGGATGCATACAGCAGTGAATCAACTCAAGAGGTTATAGTTAACTGATCCCATGAAGCAAG 3470
| | | | |
Db 3069 CGGATGCACACGGCTGTGAAGCTCAATGGCGTCTGCTCTCAACAAAGTCCCGAGATCGCAG 3128
| | | | |
Qy 3471 CTGGTTTTTATTGAATATGCCAGGGCCACCCGAAACCTCGAGGGTGTGATGAATACATG 3530
| | | | |
Db 3129 CTGTCTCTGCTCAACATGCCAGGTCCTCCAAAACCCGCGAGGAGACGAGACTACATG 3188
| | | | |
Qy 3531 GAGTCTCTAGAGTGTCTTACCGAGGAGCTAGAGCGAGTCTTACTTGTCCGGGGTGGTGGC 3590
| | | | |
Db 3189 GAGTCTCTTGAAGTCTTACCGAGGGCTGAACAGAGTCTCTCTGTCAGGGGTGGCGGC 3248
| | | | |
Qy 3591 AGTGAAGTGTATCACCATTATTATATAA 3617
| | | | |
Db 3249 CGGGAGGTGATCACCATTACTCTCTAA 3275
| | | | |
RESULT 12
ABA09195
ID ABA09195 standard; cDNA; 5261 BP.
XX
AC ABA09195;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human K/Cl cotransporter homologue cDNA, SEQ ID NO:971.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumor; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; anti-inflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnery; antiulcer; ss.
XX
OS Homo sapiens.
XX
PN WO200157188-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US03800.
XX
PR 03-FEB-2000; 2000US-0496914.
XX
PR 27-APR-2000; 2000US-0560875.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-457740/49.
DR P-PSDB; ABB11951.
XX
XX Human proteins and DNA encoding sequences useful for preventing,
PT treating or ameliorating a medical condition in a mammalian subject
PT e.g. arthritis and cancer -
XX
PS Claim 1; Page 828-830; 1963pp; English.
XX
CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,

CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness.
CC auto-immune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a
CC novel human polypeptide of the invention.

XX
SQ Sequence 5261 BP; 1019 A; 1625 C; 1568 G; 1049 T; 0 other;

Query Match 33.2%; Score 1416.2; DB 22; Length 5261;
Best Local Similarity 66.9%; Pred. No. 0;
Matches 2104; Conservative 0; Mismatches 1010; Indels 33; Gaps 5;

QY 483 GACGACATAGAAAGCTCGAAATGCTTATCTCAATAATTCATAAGAGAGAT 542
DB 150 GATGAATCCAAAGAGAAAGAGCCATTCCTCAACATGTCGAGTGGACAGAGAGC 209
QY 543 GAATATTTGATAAAATTTGGCACTTTTGAGGAAGAAATGGACACCGAAGGTG 602
DB 210 TTCTTTGAAGGGAAGAAATGCACTTTTCGAGGAGGAGATGACAGTAAACCCATG 269
QY 603 TCTTCCCTCTCAACCGCATGGCCAAATTAACATATCTGACTCAAGGAGCAAGAAAT 662
DB 270 TCCTCGCTGCTCAACAAGCTGGCCAACTACACCAACCTGAGCCAGGGCGTGGTGAGC 329
QY 663 GAAGAGGCGAAGAAACATCACTCAAGGGAAGAAAGAGCCACCAAGACCCCAATGGT 722
DB 330 GAGGAGGACGAGAGAGCGCGCGGGA-----GGCCNAGGCTCCGCGCATGGGC 380
QY 723 ACCTTCATGGGTGTCTACCTCCCATGTCTCAAAAATATTTTGGAGTGATCTCTTTT 782
DB 381 ACCTTCATGGGTGTCTACCTCCCATGTCTCGAGAACATCTCTGGCGTCTCTCTCTG 440
QY 783 CGCCTTACATGGGTGGTGGGACAGCTGGAGTTCTTCAGGCTTTTGGCAATTCCTATC 842
DB 441 CGCCTGAGCTGGATCGTGGGGGTGGTGGTGTCTCTGAGTCTCTCTCATCTGGCCATG 500
QY 843 TGCTCTGCTGTACAAATGTTGACTGTATCTCCATGAGTGCCATTTGCCAATATGAGTG 902
DB 501 TGCTGCACATGTACAAATGTTGAGCCCATTTCCATGAGTGGCATCGCTACCAACGGTGT 560
QY 903 GTGCCAGCTGGGGGTCTACTTTATGATTTCCCGGGCACTGGGCCACAGAGTTTGGTGG 962
DB 561 GTCCCAGCTGGGGGTCTCTACTACATGATATCGCGCTCGCTGGGACCGAGTTTGGAGC 620
QY 963 GCTGTTGGCCTCTGCTTTTATCTTGGTACCACATTTTGCAGAGCCATGTACATCCTGGT 1022

DB 621 GCTGCGCCCTCTGCTTCTTACTCTGGGCACGAGTTTGCAGGGGCCATGTATATTTGGGG 680
QY 1023 GCCATTGAAATCTTTCTGGTCTATATCTGCCCCAGCTGCCATCTTTACAGATGATGAC 1082
DB 681 ACCATCGAGATTTTCTGACGTACATCTCCCGGGTGGGCCATCTTCCAGGGGAGGCT 740
QY 1083 GACTCAAGGAATCAGACGCAATGTAATAACATGCGTGTCTACGGCACAGCTTTCTTTG 1142
DB 741 GCAGGTGCGAGGCGCGGCCCATGTGTCACAAATGTCGTCGCTGTATACGGCACGTCACGCTC 800
QY 1143 GTCCTTATGATATAGTGGTATTTATCGGCTACGCTATGTGAACAAGTTTGCCTCANTT 1202
DB 801 GTGCTCATGGCCCTGGTGGTCTTCTGGGCGTCAAGTATGTCAACAAGTGGCGGTGGTC 860
QY 1203 TTCTGGGCTGTGTCTTGTCTTCCATCTTGGCCATCTATGTGGAGCCATCAAGTCTTCT 1262
DB 861 TTCTGGGCTGGTGGTGTGTCTTCCATCTTGGCCATCTATGCGGCGTCTCAAGTCTGGC 920
QY 1263 TTGCTCTCTCACACTTCCCGTCTGCAATGCTGGTAAACCGCACTCTTTTCATCAAGAC 1322
DB 921 TTGCAACCCCGGACATCCCGTCTGCTCTGCGGAAACCGCACGCTGTACGGGCGAGC 980
QY 1323 ATTGACGTTTCTCTTAAGACCAAGAAATTAACACATGACAGTCCCATCAAGTATGG 1382
DB 981 TTGATGCTGCTGCTCAAGGCTTACGGCATCCACAACTCAGCCACCTCCGCGCTCTGG 1040
QY 1383 GGATTTCTCTGTAATCTGAGTCAATTTTCAATGCACTGCTGATGAATACTTTGTTCAC 1442
DB 1041 GGCCTCTTCTGCAACGGCTCCCA---GCCAGCGCGCTGTGACGAGTACTTTCATCAG 1097
QY 1443 AATAACGTCACCTCAATCCAGGCACTTCTCGATTTGGTGTAGTGTATTAATACAGAGAT 1502
DB 1098 AACACGTCACCGAAATCCAGGCACTCCGGCGCGGCGAGTGGTGTCTTCTCGGAGA 1157
QY 1503 CTTTGGAGTATTAACCTACCCCAAGGGAGAGATCATCGAAA-----GCCTTCAGCC 1553
DB 1158 CTGTGGAGTACGTACGCGCACGCGGGGCGTGTGTGGAGAGAAAGGTGTGCCCCCTGGTG 1217
QY 1554 AATCTCTGATGTCTTATAGGAGCTTAAACCATGAATATGTTTGTGTGACATCAACACC 1613
DB 1218 CCGTGGCAGAGGAGAGCGGTCACGACACATGCCCTAGTGCTCACGACATCCGGGCC 1277
QY 1614 TCCTTCACGCTTCTGGTGGAAATCTTTTCCCTCTGTTACAGGTATCATGCTGGATCA 1673
DB 1278 TCTTCACTCTGCTGGTTGGCATCTACTTCTCCGTGACCGGTATCATGSCGGGTCA 1337
QY 1674 AACAGATCTGAGATCTGAAAAGATGCTCAGAAAGTCTATTCGATTTGGTACTATCTCTGC 1733
DB 1338 AACCGGTCCGGGACCTCAAGGATGCACAGAAAGTCCATCCCAACGGGACCATCTCTGGCC 1397
QY 1734 ATCTGACCACTCTCTTTGTTTATTAAGCAATGTTGTCTTTTGGTGTGATGATGAA 1793
DB 1398 ATAGTACAGAGCTCTTTTCATCTATCTCTCTGCAATGTGCTTTTGGGGCTGCAATGAA 1457
QY 1794 GGGGTGTCTCTCAGACAGCAAGTTCGGTGATGCTGTGAAGGTAAATTTGGTGTAGGACCC 1853
DB 1458 GCGGTGTCTTACAGATAAGTTCGGGAGGCCCTGACAGGGGAACCTGCTCATCGCATG 1517
QY 1854 TTATCTTGGCCATCCCATGGGTGATTTATTTGGTCTCTTCTTTTCAACATGTGGGGCT 1913
DB 1518 CTGGCTCTGGCCCTCCCTCTGGGTCTATCTCATCGGCTCTCTTCTTCTCACCTCGGGTGC 1577
QY 1914 GGACTTCAGAGCCCTCAGAGTGACCGAGGCTGTACAAGCTATTTCGCAAGCAATAACATC 1973
DB 1578 GGCCTGACAGCCCTCAGGGGGCACCGGCTCTACTGAGGCCATTTGCCGTGACGGCATC 1637
QY 1974 ATACCGTTCTGAGGGTTTTTGGCCACAGCAAGCAATAGGGGAACCTTACCTGGGCTTTA 2033
DB 1638 GTCCCTCTCTGCAAGTGTGTGGCCACGGGAAGCCACAGGGAGCCACCGTGGGCGCTG 1697
QY 2034 CTTCTAATCTGCTGCATTTGACAGCTTGGAAATATCTATTTGCTCTCTCTGATCTTTGTG 2093

Db 1698 CTGCTGACAGTCTCATCTGCGAGACTGGCATCTCTATCGCCTCTCTGGACACGCTGGCC 1757
Qy 2094 CAAATCTTTTCCATGTTTTCTCATGTGTATACCTCTTTGTAAACTTGGCATGTCCCTTG 2153
Db 1758 CCGATCCTCTCCATGTTCTCTCATGTGTACCTACCTTGTGTAACCTGSCCTTGCCTG 1817
Qy 2154 CAAACATTTACTTCGAACACCCAACTGGAGACCCCGATTCCGCTACTACCATTTGGGCCCTT 2213
Db 1818 CAGACCTCTACTAGTACCCCACTGGCGTCCACGCTTCAAGTCTTACCACTGGACCTG 1877
Qy 2214 TCTTTCATGGGAATAGATATCTGTCTGGCTCTGATGTTCAATTTCTTCTGGTATATGCC 2273
Db 1878 TCTTTCTGGGTATGAGCCTGTGCTTGGGCTGATGTTCACTGTCTCTGTGTAACGCG 1937
Qy 2274 ATTGTAGCACAAGTATAGCTGATGATCAAGTACATTAAGTAAATCAACAGAGCTGAG 2333
Db 1938 CTGTCCGCCATGCTCATCGCTGGCTGCTCAAGTACATCGATGACCGGGGCCGAG 1997
Qy 2334 AAAGAAATGGGGTATGTTATCCGTGGGCTGTCCCTCAGTGCAGCCCGGTTTCTTTGCTT 2393
Db 1998 AAGGAGTGGGGCATGGCATCGTGGCTTATCCCTGAACGCCCGCTACGCCCTGCTG 2057
Qy 2394 CAGATTGGAGAGGACCTCAACACATAAACTGAGAGCCCTCAGTTGCTGTGTTATATCTG 2453
Db 2058 CCGGTGGAGCAGCTCCCGCCACACCAAGAACTGGAGGCCCGCAGGTGCTGTGATGCTG 2117
Qy 2454 AAATAGATGAGACTTACATGTCAAGCATCTCGCCTCTCACCTTTGCTCCCTCACAGTCT 2513
Db 2118 AACCTGGACGGGAGCAGGCATGAAGCACCCCGCTCTGTCTTCTACGTGCGAGCTG 2177
Qy 2514 AAAGCAGGAAAGGTTACTATTGTGGGCTCTGTCTCATCTGTGGGAACTTCTCTAGAGAAC 2573
Db 2178 AAGCCCGCAGAGGCTGACCATCTGGCTCGTCTGGAGGAGCTACCTGGACAG 2237
Qy 2574 TAGCGTGAAGCTTTAGCTGTGAGCAGACATAAAGCACTAATGAGGAGCAGAGAGTGA 2633
Db 2238 CACATGAGGCTCAGCGGGCGGAGGAGAACATACGGTCTCTTATGAGCAGACAGAGAC 2297
Qy 2634 AAGGATTCCTGCAGCTGGTGGCGCCAGCTCAGAGAGGGCATTTCCACCTCATC 2693
Db 2298 AAGGCTTCTGCAGCTGGTGGTCTCTGTCAGCCTCGGGATGGCATGTCCTCCACCTGATC 2357
Qy 2694 CAGTCATGTGGCTTGGGGCATGAAGCAACAACCGTGTGTGATGGGCTGGCCTAATGGC 2753
Db 2358 CAGTCGGCGCTTGGGGCTTGAAGCAACAACCGTGTGTGATGGGCTGGCCTGATCC 2417
Qy 2754 TGGCGTCAAGAGCAAGATGCCCGCTTGAAGACTTTTATTTGGCACAGTTGAGTGAACA 2813
Db 2418 TGAAGCAGGAGGACAAACCCCTTCTCTGGAAGAACTTTGTAGACACCGCTCCGCGACAC 2477
Qy 2814 ACTGCTGCCATCTTGCACCTGGTGGCTAAGCAATCTCTCTTCTCCAGCAATGTG 2873
Db 2478 ACCGCGCGCACCAGGCTCTGCTGGTGGCCAGAACGTGCACTCGTTTCCGCAAAACCA 2537
Qy 2874 GAGCAATTTTCTGAGGCAACATTTGATGTGTGGTATTTGTCATGATGGGGGATGCTT 2933
Db 2538 GAGGCTTCGGCGGGGCACTCGACGTGTGTGGTCTGTGCAACGAGCGGCGATGCTC 2597
Qy 2934 ATGCTACTACATTTCTTCTAAGAACAGCAACAAGTGTGGGAAAGTGCAGCATACGGATC 2993
Db 2598 ATGCTGCTCCCTTCTCTGCTGCGCAGCAACAAGTGTGGAGGAAGTGCAGGATGCTATC 2657
Qy 2994 TTCACAGTACCCAAATTTAGAGACACAGTATCCAAATGAAGAGGACCTAGCACCTTC 3053
Db 2658 TTCACGCTGGCCAGGTGGACGACCAACAGCATCCAGATGAAGAGGACCTGCGAGATGTT 2717
Qy 3054 CTATATCACTTACGCAATTTAGGGGAGGTAGAAGTGTGAGATGTCATGACAGTATAT 3113
Db 2718 TTGTACCACTTGGCATCAGCGCGAGGTGGAGTGTGTGAGATGTTGTAACACGACATA 2777
Qy 3114 TCAGCATATATCTTACGAGCGCACTTTTGTATGATGAACAAGGTCCTCAGATGCTTCGGCAC 3173
Db 2778 TCTGCTTTCACCTACGAGAGGACACTAATGATGAGCAGAGGTGCGAGATGCTGAAGCAG 2837

Qy 3174 ATGGCGCTATCCAAAAACAGACGAGACAGAGGCACAATTTGGTGAAGACCGAAACTCA 3233
Db 2838 ATGCAGCTGTCCAAAGAACGACGAGGCGAGAGGCCAGCTGATCCACGACAGGAACACC 2897
Qy 3234 ATGTACGATTGACAGCAITTTGGCTCTGTATGAGGACGAGAGACAGAAACCTATCAGGAG 3293
Db 2898 GC-----GTCCACACCGCGCGGCGAGCCAGGACCCAAAGCGCGCCTTACGCCAGAC 2948
Qy 3294 AAGTGCACATGACTTGGACAAAAGACAAAGTACATGGCATCCCG- ---GGACAAAAGCG 3350
Db 2949 AAGTGCAGATGACTTGGACCCAGGAGAAAGCTGATCGCTGAGAAGTACAGGAGCAGAGAC 3008
Qy 3351 AAGTCAATGGAAGGATTCAGGACCTGTTAAACATGCGTCCGGAACAGTCCAATGTGAGG 3410
Db 3009 ACCAGCCTATCTGGTTTCAAGACCTCTTCAAGCATGAAGCCGACCACTCCAACGCTCAGG 3068
Qy 3411 CGGATGCATACAGCAAGTGAACCTCAACGAGGTTATAGTTAAAGTCCATGCAAGCAAG 3470
Db 3069 CGGATGCACACGGCTGTGAAGCTCAATGGCTGCTCTCAACAAGTCCAGGATCGCAG 3128
Qy 3471 CTGGTTTTTATTTGAATATGCCAGGGCCACCCGAAACCTGAGGGTGTATGAAGAACTACATG 3530
Db 3129 CTGGTCTCTGCTCAACATGCCAGGCTCTCCAAAACCCGAGGAGACGAGAACTACATG 3188
Qy 3531 GAGTTCTCTAGAGGTGCTTTACCGAGGGAAGTACAGCGAGTCTTACTTTGTCGGGGTGTGGC 3590
Db 3189 GAGTTCTTGAAGTCTGACCGAGGGGCTGAACAGAGTCTCTCTGTCAGGGGTGGCGC 3248
Qy 3591 AGTGAAGTATCACCATTATTATATAA 3617
Db 3249 CGGGAGGTGATCACCATCTACTCTTAA 3275

RESULT 13

AAS59393
ID AAS59393 standard; cDNA; 5155 BP.

XX AC AAS59393;

XX DT 16-JAN-2002 (first entry)

XX DE Mouse cDNA encoding potassium-chloride cotransporter KCC4.

XX KW Mouse; ss: potassium-chloride cotransporter; epilepsy; hypertension;
KW KCC; hypotensive; anticonvulsant; antianaemic; sickle-cell anaemia;
gene therapy.

XX OS Mus sp..

XX PN WO200179525-A2.

XX PD 25-OCT-2001.

XX PF 16-APR-2001; 2001WO-US12395.

XX PR 14-APR-2000; 2000US-197350P.

XX XX (UYVA-) UNIV VANDERBILT.
XX (GAMB/) GAMBIA G.

XX PI Gamba G, Mount DB, Delpire E, George AL;

XX DR WPI; 2001-611726/70.

XX DR P-PSDB; AAU39098.

XX PT New isolated and purified potassium-chloride cotransporter polypeptide
PT for detecting a modulator of potassium-chloride cotransporter that can
PT treat epilepsy, sickle cell anaemia, and hypertension -

XX PS Claim 24; Page 279-287; 352pp; English.

XX CC The invention relates to an isolated and purified, biologically active

CC KCC2, KCC3, or KCC4 potassium-chloride cotransporter polypeptide
 CC and polynucleotides encoding them. KCC and the nucleic acid encoding KCC
 CC are used to produce an antibody against KCC, which can be used to detect
 CC KCC. The antibody and nucleic acid are used in kits to detect KCC and
 CC the nucleic acid encoding KCC. KCC and nucleic acid encoding it are used
 CC to screen for candidate substances that can modulate the activity of KCC.
 CC KCC and the nucleic acid encoding it can be used to modulate potassium-
 CC chloride cotransport in a vertebrate. Therapeutic compositions
 CC comprising modulators of the activity of KCC (preferably antibodies or
 CC antisense oligonucleotides) are used to treat epilepsy, sickle cell
 CC anaemia, and hypertension (also via gene therapy using the KCC
 CC polynucleotide). The present sequence encodes a KCC of the invention.
 XX
 SQ Sequence 5155 BP; 1135 A; 1414 C; 1388 G; 1212 T; 6 other;

Query Match 33.2%; Score 1415; DB 22; Length 5155;
 Best Local Similarity 67.0%; Pred. No. 0;
 Matches 2092; Conservative 0; Mismatches 998; Indels 33; Gaps 5;

QY 508 CTTATCTCAATTAATTCATATGAGAGGAGATGAATATTTTGTATAAATTTGGCAC 567
 DB 224 CTTTCATCAATTAATTTGGAGTGGAAAGAGAGAGCTACTTCGAGGGGAAACATGGCAN 283
 QY 568 TCTTTGAGGAAGATGGACACAGCCAGCCAGGTCTTCCCTCTCAACCCGATGGCA 627
 DB 284 TTTTGGAGGAGATGGACAGCAACCCATGGTGTCTACTGTCTGAAACAGCTGGCA 343
 QY 628 ATTACACTAATCTGACTCAAGGAGCAAGGAACATGAAGAGGAGCAAAACATCACTGAAG 687
 DB 344 ACTATACCAACCTGAGCCAGGTGTGTAGACATGAGGAGATGAGGACA----- 394
 QY 688 GAAAGAGAGCCCAAGACCCCAATGGGTACCTTCAATGGGTGTCTACCTCCAT 747
 DB 395 GCGGAGGCGAGAGGTCAAGGCCCAACGATGGGCACTTATCGGAGTCTACCTGCCGT 454
 QY 748 GTCTACAAATATTTTGGAGTGATCTTTTACGGCTTACATGGGTGGGGCAG 807
 DB 455 GCTCGAGAAATCTTTGGGTGTATCTTTTCTCGCTGTGACCTGGATTTGGGGGCGAG 514
 QY 808 CTGAGGTCTTTCAGGCTTTTCAATTTGCTTTATCTGCTGTCTGTATCAATTTTGACTG 867
 DB 515 CTGTGTATGAGGCTTCTTCATTTGTCATTTGTCATGTCATGTCATGTCATGTCATG 574
 QY 868 CTATCTCAATGATGCCATGTCATTAATGAGTGGTGGCCAGTGGGGCTCATACTTTA 927
 DB 575 CCATCTCAATGAGCCCATCGCTACCAAGCGGTGGTCCAGCGGGAGGCTCGTACTACA 634
 QY 928 TGATTTCCGGGCACTGGCCAGAGTTTGGTGGGGCTGTGGGCTCTGCTTTTATCTTG 987
 DB 635 TGATCTCCGCTGCTGGGGCTGAGTTGGAGGTGCTGTTGGCCCTCTGCTTCTACTTGG 694
 QY 988 GTACCACATTTGACGACGATGATCATCTTGGTGGCCATGAAATCTTTCTGGTCTATA 1047
 DB 695 GCACGACATTTGACGGCCGATGATCATCTTGGGTACCATCGATCTTCTGACCTACA 754
 QY 1048 TCGTCCCGGAGCTGCCATCTTTACAGTGTAGTACGCACTCAAGGAATCAGCAGCATGC 1107
 DB 755 TCTCTCCAAGTGGGCCATCTTCCAGGCGAGAGACGGGGGATGGCGCGCGCACTGT 814
 QY 1108 TAAATAACATGGTGTCTACGGCAGAGCTTTCTTGGTCTTATGTATAGTGTATTTA 1167
 DB 815 TGAACAACATGGTGTATGGCAGCTGTGCCCTGGCACTATGGCGGTGGTGTCTTTG 874
 QY 1168 TCGGGTACGCTATGTGAACAGTTTGTCTCATNTTTCTCGCCCTGTCTATTGTGCTCA 1227
 DB 875 TTGTGTCAATATGTCAACAGCTGGCACTGGTCTTCTTAGCCTGTGTGTGCTTTCTA 934
 QY 1228 TCTTGGCCATCTATGCTGGAGCCATCAAGTCTTTTGTCTCTCCACACTTCCCGGTCT 1287
 DB 935 TCTTGGCCATCTATGCTGCTGTCTATCAAGACAGCTTTGGCCCACTGACATCCGGTCT 994
 QY 1288 GCATGCTGGGTAAACGCACTCTTTTCATCAAGACACATTTGAGCTTTGCTTAAGACCAAG 1347

DB 995 GCCTTCTAGGAAACGGCAGCTGGCAATCGCAATCTTGATACCTGTGCCAAGATGCAGG 1054
 QY 1348 AAATTAACAACATGACAGTCCCATCAAAAGTTATGGGATTTCTTGTAACTCGAGTCAAT 1407
 DB 1055 TTGTGAGCAACGGTACAGTACCACTGACACTCTGGCGCTCTTCTGCAATG--GCTCCA 1111
 QY 1408 TTTTCAATGCCACCTGTGATGAATACTTTGTTTCAATAAGTCTACTTCAATTCAGGGCA 1467
 DB 1112 GCTTGGGTGCCACCTGTGATGAGTACTTTTGACAGAAACAAGCTTACTGAGATACAGGCA 1171
 QY 1468 TTTCTGGATTTGGCTAGTGTGATTAATACAGAGAAATCTTTGGAGTAATTTACCTACCCAAAGG 1527
 DB 1172 TCCCTGGTGTGGCAGTGGTGTCTTCTCGATTAACCTGTGGAGACATATTCAGACAAG 1231
 QY 1528 GAGAGATCATCGAAAA-----GCCTTCAGCCAAATCTTCTGATGTCTTAGGCAGCT 1578
 DB 1232 GGGCATTTGTGAAAAAGAAAGGTGTCTCAGTGCCTGTGTCCGAGGAGAGCGGCTG 1291
 QY 1579 TAAACCATGAATATTTCTTGTTCACATCACCACTCTCTTCAAGCTTCTGGTGGGAATCT 1638
 DB 1292 GTGATTTGCCATACGTCTCTCAAGACATCATGACCTACTTCCACCATGTAGTTGGCATCT 1351
 QY 1639 TCTTTCCCTCTGTACAGGTATCATGGCTGGATCAAAACAGATCTGGAGATCTGAAGAATG 1698
 DB 1352 ACTTCCGCTGTAACTGGGATCATGGCAGATCAACCGCTCCGGGACCTCAAGAGC 1411
 QY 1699 CTCAAGAGTCTATTTCCGATTTGCTACTTCTTGGCATCTGACCACTCTCTTTGTTTAT 1758
 DB 1412 CCCAGAGTCTATTTCCAAAGGACCATTTGGGCCATCTGACCTACATCTTTTATTATN 1471
 QY 1759 TAAGCAATTTGTCCTTTTGGTGCATGATTTGAAGGGTGTGTTCTCAGAGACAAGTTG 1818
 DB 1472 TTTCTCTGATAGTGTCTTTTGGGCTGCAATGAAGGTGTAGTCTCTCGAGATAAGTTG 1531
 QY 1819 GTGATGTGTGAAGTAATTTTGGTGTAGGACCTTATCTTGGCCATCCCAATGGGTGA 1878
 DB 1532 GGGAGGCTTTCGAAGGAAACCTGTGTCATTTGGCTGGCCATCTCCCTGGGTGCA 1591
 QY 1879 TTGTATTTGGCTCTCTTTTCAACATGTGGGGTGGACTTTCAGAGCCTCACAGTGCAC 1938
 DB 1592 TTGTGATTTGGCTCTCTTCTTCCACTGTGTGTGTGGCTGCAGAGCCTGACTGGGCA 1651
 QY 1939 CGAGGCTCTACAGCTATTTGGCCAAGGATAACATCATACCTTTCTGAGGGTGTGTTGGCC 1998
 DB 1652 CCCGCTACTGACAGCCATTTGGCGGTGACGGAATCATCCCCCTCTACAGGTGTGTTGTC 1711
 QY 1999 ACAGAAAGCAATGGGGAACTACCTGGGCTTTACTTCTAACTGCTGCCATTCAGAGC 2058
 DB 1712 ATGAAAGGGCCACCGGGAGCCCATGCGGCTGTCTGCTCACGGCTCTCATCTGTGAGA 1771
 QY 2059 TTGGAATACTCATTTGCTCTCTGATCTTGTGGCCCAATTTCTTCTCAATGTTTCTTCA 2118
 DB 1772 CCGGTATCTCATGCTCTCTCTGACAGTGTGGGCCCCCATCTCTGTCCATGTTCTTNTCA 1831
 QY 2119 TGTGTTACCTCTTTTGAATTTGGCATGTGCTTTGCAAAACATTAATTCGAACACCCAACT 2178
 DB 1832 TGTCTACATGTTGTCATCTGSCCTGTGCGGTACAGACCTGCTACGCAACCCAACT 1891
 QY 2179 GGAGACCCGATTCGGCTACTACCATTTGGGCCCTTTCTTTTCATGGGAATGATGATCTGTC 2238
 DB 1892 GCGTCCACGCTTCAAGTTCTACCACTGGACCTCTCTCTCTCTTGGGATGATGCTCTGCC 1951
 QY 2239 TGGCTCTGATGTTTCAATTTCTTCTGTTATTTATGCAATTTAGCCATGATGATAGTGTA 2298
 DB 1952 TCGGCTGATGTTTCAATCTGCTCTCTGTTACTACGCCNTTTTTCGCCATGCTCATTTGCCGCT 2011
 QY 2299 TGATCTAAGATACATTTGAATACCAAGAGCTGAGAAAGATGGGGTGTATGTTATCCGTG 2358
 DB 2012 GCATCTAAGATACATCGAGTACCGCGGCTGAGAGGAGTGGGGGATGSCATCAGG 2071
 QY 2359 GGTGTCTCTCAGTGCAGCCGGTGTGTTGCTTTCGATTTGGAGGAAGGACCTCCACACA 2418
 DB 2072 GCCTGTCACTGAATGCTGCCCGCTACGCCCTGTGCTGCGTGTGGAAACATGGGCCCCACATA 2131

Qy	2419	CTAAAACTGGAGGCCTCAGTTGCTTGTATTA	CTAGTAACTAGATGAAGACTTACATGTCA	2478
Db	2132	CCAAGAACTGGAGGCCCCAGGTGTGTGATGCTGTAACCTGGACTCGGACGAGTGTGTA	2191	
Qy	2479	AGCATCTCGCTCCTCCTCACCTTTGCCCTC	CAGCTCAAAGCAGGAAAAGGTTTACATATTG	2538
Db	2192	AGCACCCCGCTCTGCTCTCTTCACTCTCAGCTGAAGGCTGGCAAGGGCTGACCATCG	2251	
Qy	2539	TGGCTCTGTCATCGTGGGGAACCTTC	TAGAGAACTACGGTGAAGCTTTAGCTGCTGAGC	2598
Db	2252	TGGGATCTGTCTAGAGGCAACCTACTTT	TAGACAAGCATGTGGAGGCCCAGAGGCTGAAG	2311
Qy	2599	AGACATAAAGCACCTAATGAGGCGAGAGAGGTAA	AGGATTTCTGCCAGCTGTGTGGTGG	2658
Db	2312	AGAATATCCGCTCTCTGATGAGTGCAGAGAAGACGA	AGGAGGCTTCTGCCAGCTGTGTGTGT	2371
Qy	2659	CGGCCAAGCTGAGAGAGGCAATTTCC	CACTTCAGTCAATGTGGGCTTGGGGGCATGA	2718
Db	2372	CCTCCAACTCGAGAGATGGTCCGTCCCACTGATCC	AGTCCAGTCCGCTGGCTCGTGGCATGA	2431
Qy	2719	AGCACACACGGTGTGATGGCTGGCTTAATGCT	GGCGTCAAAAGCAAGATGCCCGCG	2778
Db	2432	AACACAACACTGTCTCTATGCGCTTGGCCAGAGGCTT	TGGAAGGAGGAGATAAATCTTTCT	2491
Qy	2779	CTTGGAAACATTTTATTTGGCACAGTTCG	AGTGAACAATGTCTGCCATCTTTGCACTGCTGG	2838
Db	2492	CTTGGAGAACTTTGTAGACACAGTCCGTGACAT	ACAGCAGCACATCAGGCTTTGTGG	2551
Qy	2839	TGGCTAAAAACATCTCCTTTCCCAGCAATGT	GSAGCAATTTTCTGAGGGCAACATTG	2898
Db	2552	TGGCCAAGAACATTGACTTATTTCCACAAA	ACCAAGAGCGCTTCAGCGACGGGAACATTG	2611
Qy	2899	ATGTGTGTGTGATTTGTGCATGATGGGGGAT	GCTTTATGCTACTACCAATTTCTACTGAAC	2958
Db	2612	ATGTGTGTGTGATCGTGCATACAGGGGGCAT	GTCTCATGCTTCTGCCCTTTCTGCTGCGCC	2671
Qy	2959	AGCACAGGTGTGCGAAAGTGCAGCATACGG	ATCTTACAGTAGCCCAATTTAGAAGACA	3018
Db	2672	AGCACAGGTGTGCGGAAAGTGC	CGGATCGCATCTTCACTGTGGCCAGGTGGATGA	2731
Qy	3019	ACAGTATCCAAATGAAGAAGACCTAGCC	ACCTTCTTATATCACTTACGCATTTGAGCGCG	3078
Db	2732	ACAGCATCCAGATGAAGAAGACCTGCAGAT	GTGTTCTGTACCACCTCAGGATCAGTSCCG	2791
Qy	3079	AGGTAGAAGTGGTGAGATGCATCAGAGT	GTATATCAGCATATCTTACGAGCGCACTT	3138
Db	2792	AGGTGGAGGTGGTGAGATGGTTGAAAT	TGATATTTCCGCAATTCACCTATGAGAAGACGC	2851
Qy	3139	TGATGATGGAACAAAGTCCAGATGCTTT	CGGCACATCGGCTATCAAAACAGAGCGAG	3198
Db	2852	TAAATGATGGACGAGGTTCAGATGCT	TGAAACAGATGCATTTGTAAGATGAGCGGG	2911
Qy	3199	ACAGAGGCGCAATTTGGTGAAGACCG	AAACTCAATCTACGATTCACCAAGCATTTGGCT	3258
Db	2912	AGAGAGGCGCCAGCTGATTCATGAC	AGAACTGTCATCCATACACAGCAACTGCTA	2971
Qy	3259	CTGATGAGGACGAGAGACAGAAACCT	TATCAGGAGAGGTGCATGACTTGGCAAAAG	3318
Db	2972	GAAACCAAGCCCCCAACA-----	CCCGACAAAGTGCAGATGACATGGACGAAAG	3022
Qy	3319	ACAAGTACATGGCATCC--	CGGGACAAAAAGCGAGTCAATGGAGGATTTCCAGACC	3375
Db	3023	AGAACTCATTTGCAGAGAAACAGAG	AACAAGGACATGGGCCCATTCAGGCTTTCAAAGACC	3082
Qy	3376	TGCTTAAATCATCGTCCGACCAAGTCC	CAATGTGAGCGCGGATGCATACAGCAGTGAATCTCA	3435
Db	3083	TCTTCAGCCTAAGCCGACCCAGTCC	CAAGTCCAGCTCAGGAGGATGCATCTGCTGTGAAGTCA	3142
Qy	3436	ACGAGGTTATAGTTAAAGTCCCAT	TGAAGCAAAAGCTGGTTTTTATTTGAATATGCCAGGGC	3495
Db	3143	ACGGCGTAGTTCTCAACAAGTCC	CAGGATGCCCAACTGGTCTCTGCTGAATATGCCAGGCC	3202

Qy	3496	CACCCGAAACCCCTGAGGGTGATGAAMAACTACATGGAGTTCCTAGAGGTGCTTACCGAGG	3555
Db	3203	CCCCAAAAGTCGGCAGGGGGCAGAGAACTACATGGAGTTCTCGAGGTCTCTGACCGAAG	3262
Qy	3556	GACTAGAGCGAGTCCTACTTGTCCGGGGTGGTGGCAGTGAAGTGATCACCATTATTATTCAT	3615
Db	3263	GGCTGGAACAGGGTCTCTCTGGTCAGGGGTGGTGGCCGAGAAGTCATCACCATTACTCTCT	3322
Qy	3616	AAC 3618	
Db	3323	AAC 3325	
RESULT 14			
AAKS2651			
ID	AAKS2651 standard; cDNA; 5261 BP.		
AC	AAKS2651;		
DT	06-NOV-2001 (first entry)		
XX	Human polynucleotide SEQ ID NO 2180.		
DE	Human; cytokine; cell proliferation; cell differentiation; gene therapy;		
XX	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;		
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;		
KW	nervous system disorder; arthritis; inflammation; ss.		
XX	Homo sapiens.		
OS	WO200157190-A2.		
XX	09-AUG-2001.		
PN	05-FEB-2001; 2001WO-US04098.		
XX	03-FEB-2000; 2000US-0496914.		
PR	27-APR-2000; 2000US-0560875.		
PR	20-JUN-2000; 2000US-0598075.		
PR	19-JUL-2000; 2000US-0620325.		
PR	01-SEP-2000; 2000US-0654936.		
PR	15-SEP-2000; 2000US-0663561.		
PR	20-OCT-2000; 2000US-0693325.		
PR	30-NOV-2000; 2000US-0728422.		
XX	(HYSE-) HYSEQ INC.		
PA	Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;		
XX	Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;		
PI	Xue AJ, Yang Y, Wejhrman T, Goodrich R;		
XX	WPI; 2001-476283/51.		
DR	P-PSDB; AAM79518.		
XX	Nucleic acids encoding polypeptides with cytokine-like activities,		
PT	useful in diagnosis and gene therapy -		
XX	Claim 1; Page 4544-4545; 6221pp; English.		
PS	The invention relates to polynucleotides (AAKS1456-AAKS3435) and the		
CC	encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to		
CC	cytokine, cell proliferation or cell differentiation or which may induce		
CC	production of other cytokines in other cell populations. The		
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or		
CC	peptide therapy. The polypeptides have various cytokine-like activities,		
CC	e.g. stem cell growth factor activity, haematopoiesis regulating		
CC	activity, tissue growth factor activity, immunomodulatory activity and		
CC	activin/inhibin activity and may be useful in the diagnosis and/or		
CC	treatment of cancer, leukaemia, nervous system disorders, arthritis and		
CC	inflammation.		
CC	Note: Records for SEQ ID NO 2110 (AAKS25581), 2111 (AAKS25582) and 3666		
CC	(AAM80020) are omitted as the relevant pages from the sequence listing		
CC	were missing at the time of publication.		

XX Sequence 5261 BP; 1019 A; 1626 C; 1567 G; 1049 T; 0 other;
SQ Query Match 33.2%; Score 1414.6; DB 22; Length 5261;
Best Local Similarity 66.8%; Pred. No. 0;
Matches 2103; Conservative 0; Mismatches 1011; Indels 33; Gaps 5;
QY 483 GAGGACATAGAAAGCTCGAATGCTTATCTCAATAATTCGAATATGAAGAAGAGAT 542
DB 150 GATGAAATCCGAAGAAACAGCCATTCCTCAACAATGTGAGGTGGAACAAGAGAGC 209
QY 543 GAATATTTTATAAAATTTGGCACTCTTTAGAGGAAGAAATGGACACAGACCGAAGGTG 602
DB 210 TTCTTTGAAGGAGNAACATGGCACTTTTCGAGGAGGAGATGACAGTAACCCCATGTG 269
QY 603 TCTTCCCTCTCAACCGCATGGCCAAATTAACATTAATCTGAATCAAGGAGCAAGAAGACAT 662
DB 270 TCTCGCTGCTCAACAAGCTGGCCAACTACACAACCTGAGCAGGGCGTGGTGGACAC 329
QY 663 GAAGAGGAGAAACATCACTGAAGGGAAGAAAGAGCCACCAAGACCCCAATGGGT 722
DB 330 GAGGAGGAGGAGAGCGCGCGGGGA-----GGCCAAGGCTCCGCGCATGGGC 380
QY 723 ACCTTCATGGGTGTCTACCTCCATGCTACAAAATATTTTGGAGTGATCTCTTTTATA 782
DB 381 ACCTTCATCGCGCTTACCTCGCGTCCCTGAGAAACATCTCGGGGTCACTCTCTCTG 440
QY 783 CGCTTTACATGGGTGGTGGGCACAGCTGGAGTCTTTTCAAGGCTTTTGCATTTGCTTATC 842
DB 441 CGCCTGACGTGATCGTGGGGTGGCTGTGTCTCTGGAGTCTTCTCATCTGTGGCCATG 500
QY 843 TGCTGCTGTGACAAATGTTGACTGTATCTCCATGAGTGCCATTTGCCAATTAATGGAGTG 902
DB 501 TGCTGCACATGTACAAATGTGACCGCCATTTCCATGAGTGCATCGCTACCAACGGTGTG 560
QY 903 GTGCCAGCTGGGGCTCATCTTTATGATTTCCCGGCACCTGGGCCCGAGTTGGTGGG 962
DB 561 GTCCAGCTGGCGGTCTTACTACATGATATCGCGCTCGCTGGGACCCGAGTTGGAGGC 620
QY 963 GCTGTGGCTCTGCTTTTATCTTGGTATACCAATTTGCAGCAGCCATGTACATCTTGGT 1022
DB 621 GCTGTGGCCCTCTGCTTACCTGGGCAGCAGCTTTTGCAGGGCCATGTATATTTGGGG 680
QY 1023 GCATTTGAAATCTTTCTGTGTCTATATGTCCTCCGAGCTGCCATCTTTACAGTATGAC 1082
DB 681 ACCATCGAGATTTTCTGACGTACATCTCCCGGGTGGCGGCATCTTCAGGCGGAGCT 740
QY 1083 GCACATCAAGGAATACGAGCCATGCTAAATACATGCGGTGTAGGCGACAGCTTTCTTG 1142
DB 741 CGAGTGGCGAGCGCGCCCATGCTGCACAACATGCGGTGTACGGCACTGTCACGCTC 800
QY 1143 GTCTTATGTTATAGTGTATTTATCGGCGTACGCTATGTGAACAAGTTTGCCTCANTT 1202
DB 801 GTGCTCATGGCCCTGTGTGCTCTCGTGGCGTCAAGTATGTCAACAAGCTGGCGTGTG 860
QY 1203 TTCCTGGCTGTGTCATGTGTCCATTTTGGCCATCTATGTGGAGCCATCAAGTCTTCT 1262
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QY 1263 TTTGCTCTCCACACTTCCCGTCTGCATGCTGGGTAAACCGACCTTTTCATCAAGACAC 1322
DB 921 TTCGACCCCGGACATCCCGTCTGCTCTGCGGGAACCGCACGCTGTACGGCGCAGC 980
QY 1323 ATTGACGTTTGTCTAAGACCAAGAAATTAACAACATGACAGTCCCATCAAAAGTTATGG 1382
DB 981 TTCGATGCTGCTCAAGGCTTACGGCATCCACAACAACACTAGCCACCTCCGCGCTGTG 1040
QY 1383 GGAATCTTTCTGTAACTCGAGTCAATTTTTCATATGCCACCTGTGATGAATCTTTGTAC 1442
DB 1041 GGCCTCTTCTGCAACGGGTCCCA---GCCACGCGCGCTGTGACGAGTACTTTCATCCAG 1097
QY 1443 AATACGCTCACTTCAATCCAGGGCATTTCTGATTTGGCTAGTGGTATTAATTAACAGAAAT 1502

DB 1098 AACAACTGTCGGAATCCAGGGCATCCGCGCGCGGCGCAGTGGTGTCTTCTTGAGAAC 1157
QY 1503 CTTTGGAGTAATACCTACCAAGGAGAGATCATCGAAAA-----GCCTTCAGCC 1553
DB 1158 CTGTGGAGTACGTACGCGACGCGGGGCGTGTGTGGAGAAAGAAAGGTGTGCTCGGTG 1217
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DB 1218 CCGTGGCAGAGGAGAGCGCGTGCAGCACACTGCGCTACGTGCTCACGACATCGCGGC 1277
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DB 1278 TCCCTTACCTGCTGCTGGCATCTACTTCCCTTCCGTGACCGGTATCATGGCGGTCA 1337
QY 1674 AACAGATCTGAGATCTGAAAAGATGCTCAGAAGTCTATTCCGATTTGGTACTATCTTGC 1733
DB 1338 AACCGGTCCGGGACCTCAAGGATGCAAGAAGTCCATCCCACGGGACCATCTCTGGCC 1397
QY 1734 ATCTGACCACTCTCTTGTATTATTAAGCAATGTGTCTCTTCTTGTGTGATGATTTGAA 1793
DB 1398 ATAGTGACGAGCTCTTTCATCTATCTCTCTGCAATTTGTGCTTTTGGGCCCCGTGCAAT 1457
QY 1794 GGGGTGTTCTCAGAGCAAGTTCGGTGATGCTGTGAAGGTAAATTTGGTGTAGGCACC 1853
DB 1458 GCGTGTGCTTACAGATAAGTTTCGGGAGGCGCTGACAGGGAACTCTGGTATCGGCATG 1517
QY 1854 TTATCTTGGCCATCCCATGGGTGATTTATTTGGTCTCTCTTTTCAACATTTGGGGCT 1913
DB 1518 CTGGCTGGCCCTCCCGCTGGGTCTATCTGTCATCGCTCTCTCTCTCTCACCTGGGTG 1577
QY 1914 GGACTTCAGAGCTTCAGAGTGACCGAGGTGCTACAAGCTATTTGCCAAGGATTAACATC 1973
DB 1578 GGCCTGCAGACCTTCAGGGGCGCACCGCGCTACTGCAAGGCCATTTGCCGTGACGGCATC 1637
QY 1974 ATACCGTTCTGAGGGTTTTTGGCCACAGCAAGCAATGSGGAACCTTACCTGGGCTTTA 2033
DB 1638 GTCCCTTCTCTGAGGTGTTTTGGCCACGGGAAGGCCAACGGGAGCCCACTGGTGGCGTG 1697
QY 2034 CTTCTAACTGCTGCATTTGACAGCTTGGAACTACTCAATTTGCTCTCCCTGGATCTTGTG 2093
DB 1698 CTGCTGACAGTCTCTCATCTGGAGACTGGCATCTCTCATCTCTCTCTGACAGCGTGGCC 1757
QY 2094 CCAATCTTTCATGTTTTTTCTCATGTGTTTACCTCTTTGTAAACTTGGCATTGGCCTTG 2153
DB 1758 CCGATCTCTCCATGTTCTTCCCTCATGTGCTACCTGTTTGTGTAACCTGGCCCGTG 1817
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QY 2214 TCTTTTCATGGGAATGAGTATCTGTCTGGCTGTGATGTTTCAATTTCTCTGGTATTTATGCC 2273
DB 1878 TCCCTTCTGGGTATGAGCTGTGCTGGCGTGTGATGTTTCACTGCTCTCTGGTACTACGG 1937
QY 2274 ATTGTAGCCATGTTAATGCTGGTATGATCTACAAGTACATTTGAATACAAGGAGCTGAG 2333
DB 1938 CTGTCCGCGCATGCTCATCGCTGGTGTGATCTTACAAGTACATCGAGTACCGGGGGCCGAG 1997
QY 2334 AAAGATTTGGGTGATGTTATCCGTGGGTGTCCTCTCAGTGCGACCGCGGTTGCTTGTCTT 2393
DB 1998 AAGGATGCGGCGATGAGCATCCGTGGCTATCTCCCTGAACCGCGCCGCTACGCCCTGTG 2057
QY 2394 CGATTGAGGAAGGACCTCCACACACTAAAGCTTGGAGGCTCAGTTGCTTGTATTACTG 2453
DB 2058 CCGGTGGAGCAGCTGCCCGCCACACCAAGAACTTGGAGGCCCGAGGTGCTGTGATGCTG 2117
QY 2454 AAACTAGATGAAGACTTACATGTCAAGCATCTCGCTCTCTCACTTTTGTCTCAAGCTC 2513
DB 2118 AACCTGACGGGAGCAGGCGCATGAAGCACCCCGCGCTGCTGTCTTCTCACGCTCGAGCTG 2177
QY 2514 AAAGCAGGAAGAGTNTCACTATTTGTGGGTCTGTCTCATCTGTTGGGMACTTCTTAGAGAAC 2573
DB 2178 AAGCCCGCAAGGCGCTGACCATCTGGGTCTGGTGTGGAGGGAGCGTACCTGGACAAAG 2237

QY 2574 TACGGTGAAGCTTTAGCTCTGAGCAGACCAATAAAGCACCTTAATGAGGACAGAGAAGTGA 2633
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QY 2238 CACATGAGGCTCAGCGGCCGAGGAGAACATACGGTCCCTAATGAGCAGACAGAAGACC 2297
Db |||||
QY 2634 AAAGGATTCGACAGTGTGTGGCGCCCAAGCTGAGAGAGGGCATTTCCACCTCATC 2693
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QY 2298 AAGGGCTTCGACAGTGTGTGTCTCGTCAGCCTCGGGATGGCATGTCCACCTGTATC 2357
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QY 2694 CAGTCATGTGGCTTGGGGGCGATGAGCACACACGCTGGTGTGATGGCTGGCTAATGCG 2753
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QY 2358 CAGTCGGCGGCTTGGCGGCGCTGAAGCACACACGCTCATGCGCTTGGCGCGCATCC 2417
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QY 2754 TGGCGCTCAAGGCAAGATCCCGCGCTTGGAAAGACTTTTATGGCACAGTTTCCAGTGACA 2813
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QY 2418 TGAAGCAGGAGACAAACCCCTTCTCTGGAAGACTTTGTAGACACCGTCCGCGACACC 2477
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QY 2814 ACTGTGCCCATTTTGCACTGTGTGGCTTAAACATCTCTCTTTCCAGCAATGTG 2873
Db |||||
QY 2478 ACCGCGCGCACAGGCTCTGTGTGGCGCAAGACGTCGACTCGTTTCCGCAAAACACAG 2537
Db |||||
QY 2874 GAGCAATTTCTGAGGCAACATTTGATGTGTGGTGTGATGTGCATGTGGGGGATGCTT 2933
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QY 2538 GAGCGCTTCGGCGGGGGCCACATCGACGTTGTGTGTGATCGTGCACGCGCGCATGCTC 2597
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QY 2934 ATGCTACTACCATTTCTACTGAAACAGACCAAGGTGTGGCGAAAGTGACGATACGGATC 2993
Db |||||
QY 2598 ATGCTGCTGCCCTTCTCTGCGCCAGCACAGGTGTGGAGNAGTGCCGGATGCTATC 2657
Db |||||
QY 2994 TTCACAGTACCCAAATTGAAGACAAACAGTATCCAAATGAAGAGACCTTACGCCCTTC 3053
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QY 2658 TTCACGCTGCCCGAGTGACGACAAACAGCATCCAGATGAAGAGGACCTGCGAGATGTT 2717
Db |||||
QY 3054 CTATATCACTTACGATTCAGCGGAGGTAGAGTGTGGAGATGCATCACAGTATATA 3113
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QY 2718 TTGTACCATTTGGCATCAGCGCGGAGGTGGAGATGGTTGAAAACACACATA 2777
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QY 3114 TCAGCATATCTTACGAGCGCACTTTGATGATGGAACAAAGGTCCAGATGCTTCGGCAC 3173
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QY 3174 ATGCGGCTATCCAAACAGAGCGAGACAGAGAGGCAATTTGGTGAAGAACCGCAACTCA 3233
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QY 2838 ATGACGCTGTCCAAAGAACAGCAGGAGCGAGGCGCCAGCTGATCCACGACAGGAACCC 2897
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QY 3234 ATGCTACGATTCACGACGATTCGCTCTGATGAGGACGAGACAGAACCTTACGAGG 3293
Db |||||
QY 2898 GC-----GTCCACACCGCGCGGCGAGCCAGACCCAAAGCGCGCTTACGCCAGAC 2948
Db |||||
QY 3294 AAGGTGCACATGACTTTGGACAAAGACAAAGTACATGGCATCCCGG---GGACAAAAGCG 3350
Db |||||
QY 2949 AAGGTGCAGATGACTTGGACCGGAGAGAGCTGATCGCTGAGNAGTACAGGAGCAGAC 3008
Db |||||
QY 3351 AAGTCAATGGAAGATTCCAGGACCTGCTTAAATCCGCTCCGAGACAGTCCCATGTGAGG 3410
Db |||||
QY 3009 ACCAGCCTATCTGTTTCAAAGACCTCTTCAGCATGAAGCGGACCGAGTCCAAAGCTCAGG 3068
Db |||||
QY 3411 CGGATGCATACGACGATGAACTCAACAGGTTATAGTTAAACAGTCCCATGAGCAAG 3470
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QY 3069 CGGATGCACAGCGCTGTAAGCTCAATGGCGTCTCTCAACAAAGTCCGAGATGCGGAG 3128
Db |||||
QY 3471 CTGGTTTAAATGATGCCAGGCGCCACCCGAAACCTTGAGGGTGTATGAAACTACATG 3530
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QY 3129 CTGTCCTGCTCAACATGCCAGTCTCTCCAAAACCGGAGGAGACGAGACTACATG 3188
Db |||||
QY 3531 GAGTTCCTAGAGTGTTCACGAGGAGCTAGACGAGTCTACTTGTCCGGGTGTGTGC 3590
Db |||||
QY 3189 GAGTTCCTGAGTCTGACCGAGGGGCTGAACAGAGTCTCTCTGTGTACGGGTGCGCGC 3248
Db |||||
QY 3591 ACTGAAGTGCATCACCAATTTATTCATAA 3617
Db |||||
QY 3249 CGGAGGTGATCACCATCTACTCTCTAA 3275

RESULT 15
AAI59217
ID AAI59217 standard; cDNA; 3711 BP.
XX
AC AAI59217;
XX
DT 22-OCT-2001 (first entry)
XX
Human polynucleotide SEQ ID NO 1420.
XX
DE Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokineic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
OS Homo sapiens.
XX
PN WO20015312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
XX
P-PSDB; AAM40061.
PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
PS Claim 1; SEQ ID NO 1420; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
SQ Sequence 3711 BP; 769 A; 1039 C; 1124 G; 779 T; 0 other;

Query Match 32.8%; Score 1395.4; DB 22; Length 3711;

Best Local Similarity 69.7%; Pred No. 0;

Matches 1920; Conservative 0; Mismatches 818; Indels 15; Gaps 2;

QY 483 GACGGACATAAGAAAGCTCGAAATGCTTATCTCAATAATTCATATGAGAAGAGAT 542

Db 252 GATGGCAACCCAGGAAAGCAGTCCCTTCATCAACAGCACCAGCACAGAGAAGGGAAG 311
Qy 543 GAATATTTTGTATAAAATTTGGCACTCTTTGAGGAGAAATGGACACACAGACCCGAAGTG 602
Db 312 GAGTATGATGGCAAGAACATGCGCTTGTGAGGAGGAGATGGACACAGACCCCTATGTTG 371
Qy 603 TCTTCCCTCCTCAACCGCATGGCCAAATACACTAATCTGACTCAAGGAGCAAGAACAT 662
Db 372 TCTCCTCTGCTCAGTGGCGCTGGCCAACTACCAACCTGCCCCAGGGAAGTAGGAGCAT 431
Qy 663 GAAGAGGCAAAAAACATCACTGAAGGGAAGAAAGAGCCCAACAGACCCCAAAATGGGT 722
Db 432 GAAGAGGCAAAAAACATGAGGGTGGAAAAAGAGCCCGGTGAGGCCCAACGATGGGC 491
Qy 723 ACCTTCATGGGTGTCTACCTCCCATGTCTCAAAAAATATTTTGGAGTGATCTCTTTTATA 782
Db 492 ACCTTCATGGCGTGTACTCGCGCTGCTGCAGAACATCTTTGGCGTCACTCTCTCTG 551
Qy 783 CCGCTTACATGGGTGGGACAGCTGGAGTCTCTCAGGCTTTTGGCAATGTCCTTATC 842
Db 552 CGGCTCACCTGGGTGGTGGCAATTCAGGCATCTGAGGTCCTTCTGCAATGTTTCATC 611
Qy 843 TCGTCTGTGTACAAATGTTGACTGTATCTCCATGAGTGCCATGGCCACTAATGAGTG 902
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Qy 963 GCTGTTGGCTCTGCTTTTATCTTGGTACCAATTTGACAGCAATGACATCTCTGTT 1022
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Qy 1023 GCATTGGAATCTTCTGCTGTATCTGTCCTTCCCGGCTGCTTCCAGCTGCTTCAAGTATGAC 1082
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Qy 1143 GTCTTATGGTATAGTGTAATTAFCGGCGTACGCTATGTGAACAAAGTTTGCCTCA 1202
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Qy 1323 ATTGAGTTTGTCTTAAGACCAAGGAAATTAACAACATGACAGTCCCATCAAAAGTTATGG 1382
Db 1092 TTTGATGTCTGTGCCAAGCTGCTTTGGGAAGAAATGACAGCGTGACACACCGCTATGG 1151
Qy 1383 GAATTTCTGTAACTCGAGTCAATTTTCAATGCGCACTGTGATGAATACTTTGTTAC 1442
Db 1152 GGCCTTTTCTG---CTCCTCTCGCTTCTCAACGCCACCTGTGATGAATACTTTACCCGA 1208
Qy 1443 AATAAGCTCACCTTCAATCAGGGCAATCTCTGATTTGGCTAGTGGTATTAATACAGAGAT 1502
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Db 1449 TCTAACCGCTCTGGGACCTGAGGATGCCCAGAAAGTCAATCCCCACCTGGCACCATCTG 1508
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Db 1509 GCCATCGGCACCACTCTGCTGTCTACATCAGCTCCGTGTGTCTGTTTGGGGCTGCATT 1568
Qy 1791 GAAGGGTGTCTCAGAGACAAGTTCCGTGATGCTGTGAAGGTAATTTGGTGGTAGGC 1850
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Qy 1851 ACCTTATCTTGGCCATCCCATGGGTGATTTGTTATTTGCTCTTCTTTTCAACATGTGG 1910
Db 1629 ACTCTGGCTGGCCATCTCCATGGGTAAATGTCTCGGATCTTCTCTTCTCACTGTGG 1688
Qy 1911 GCTGACTTCAGAGCTCAGAGTGCACCGAGGCTGTACAAGCTTATTGGCAAGGATAAC 1970
Db 1689 GCTGGCTGACAGGCTCAGCGGGGCCCAACGCTGTGAGGCCATCTCGAGGATGGC 1748
Qy 1971 ATCATACCGTTTCTGAGGGTTTTGGCCACAGCAAGCAATGGGGAACCTACCTGGGCT 2030
Db 1749 ATGTGGCTCTTCTGAGGTCTTTGGCCATGGCAAGGCCAATGGAGAGCCGACCTGGGC 1808
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Db 1809 CTGCTCTGACTGCTGCTGAGATTTGGCATCTCATTTGCACTGCTCTCGACGAGGTG 1868
Qy 2091 GCCCAATCTTCTTCCATGTTTTTCTCATGTTTACCTCTTTGTTAACTTGGCATGTGCC 2150
Db 1869 GCCCCATCTCTCTATGTTCTTCTGATGCTGTACATGTTTGTGATCTTGGCTGTGA 1928
Qy 2151 TTGCAACATTTACTTTCGAACACCCAACTGGAGACCCCGATTCCGCTACTACCATTTGGGCC 2210
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Qy 2211 CTTTCTTTATGGAAATGAGTATCTGCTGGCTCTGATGTTTCAATTTCTCTGTTATTTAT 2270
Db 1989 CTCTCTTCTCTGGCATGAGCTCTGCTGGCCCTCATGTTTCATCTGCTCTGTTAT 2048
Qy 2271 GCCATGTAGCCATGTTAATAGTGTATGATCTACAAGTACATTTGAATACCAAGGAGCT 2330
Db 2049 GCATGTGTAGCCATGCTCATTTGCTGGACTCATCTACAAGTACATTTGAGTCCGTGGGCA 2108
Qy 2331 GAGAAAGAAATGGGTGATGTTATCCGTGGGCTGTCCCTCAGTGCAGCCCGGTTTGTCTTG 2390
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Qy 2391 CTTGATTTGAGGAAGGACCTTCCACACACTAAAACTGGAGGCTCAGTTGCTGTATTA 2450
Db 2169 TTACGCTTGGAGGAAGGGCCCCCACACACCAAGAACTGGAGGCCACAGCTGCTGTGCTG 2228
Qy 2451 CTGAATCTAGATGAAGTACTTACATGTCAAGCATCTCGCTCTCCTCATCTTGGCTCAG 2510
Db 2229 GTGGGTGGACCAAGACCAAGAAATGTGGTGACCCCCAGCTGCTCTCACTGACCTCCAG 2288
Qy 2511 CTAAAGCAGGAAAGGTTTCACTATTGTGGGCTCTGTCTATCTGGGGGAACTTCTCTAGAG 2570
Db 2289 CTGAAGGACGGAAGGGCTGACCATCTGGGGCTCTGTCTCTTGGAGGCACTTCTTGAA 2348
Qy 2571 AACTCAGGTGAAGCTTTAGTGTGAGCAGACCAATAAAGCACTTAATGGAGGCAAGAG 2630
Db 2349 AATCATCCACAGGCCAGCGGCGAGAGAGTCTATCAGGCGCTCTGATGGAGGCAAGAG 2408
Qy 2631 GTAAAGGATTTCTCCAGCTGGTGGCCGCCAAGCTGAGAGAGGCAATTTCCCACTC 2690
Db 2409 GTGAAGGCTTCTGCCAGGTGGTATCTCTCTCCAACTTGGCTGTGGCGGTGCCATCTG 2468

QY 2691 ATCCAGTCATGTGGCCTTGGGGCATGAAGCACAACACGGTGGTGATGGGCTGGCTAAT 2750
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Db 2469 ATCCAGTCGTGGGGCTCGGGGGCTGCAGCACAACACTGTGCTGTGGCTGGCCCGC 2528
|||
QY 2751 GGCTGGCGTCAAGCGAAGATCCCGGCTTGGAGACTTTTATTGGCACAGTTCGAGTG 2810
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QY 2811 ACAACTGCTGCCATCTTCACACTGCTGGTGGCTAAAAACATCTCTTTTCCAGCAAT 2870
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QY 2871 GTGGAGCAATTTCTGAGGGCAACATTGATGTGTGTGATTGTGCATGATGGGGGATG 2930
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Search completed: November 26, 2003, 18:09:07
Job time : 1048 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 26, 2003, 17:51:45 ; Search time 1219 Seconds
(without alignments)
11513.847 Million cell updates/sec

Title: US-09-835-976B-15
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4139.4	97.2	4215	11	US-09-835-976B-3
3	2958.8	69.5	6120	11	US-09-835-976B-7
4	2862.6	67.2	6075	11	US-09-835-976B-5
5	2732.2	64.1	6052	11	US-09-835-976B-9
6	1674	39.3	3726	10	US-09-917-800A-1667
7	1418	33.3	5239	11	US-09-835-976B-1
8	1415	33.2	5155	11	US-09-835-976B-13
9	1392.4	32.7	5907	11	US-09-835-976B-11
10	735	17.3	807	11	US-09-835-976B-110
11	613.4	14.4	2290	11	US-09-835-976B-112
12	446.4	10.5	478	11	US-09-918-995-9696
13	434	10.2	489	11	US-09-835-976B-84
14	262	6.2	1014	11	US-09-835-976B-18
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16	236.8	5.6	389	11	US-09-918-995-37681

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17	221.8	5.2	363	11	US-09-835-976B-93	Sequence 93, Appl
18	220.2	5.2	413	10	US-09-867-701-10259	Sequence 10259, A
19	201.4	4.7	323	11	US-09-835-976B-104	Sequence 104, App
20	195	4.6	423	10	US-09-960-352-1746	Sequence 1746, Ap
21	188.4	4.4	335	11	US-09-835-976B-108	Sequence 108, App
22	180	4.2	304	11	US-09-835-976B-98	Sequence 98, Appl
23	173.8	4.1	312	11	US-09-835-976B-105	Sequence 105, App
24	170	4.0	305	11	US-09-835-976B-103	Sequence 103, App
25	167.6	3.9	291	11	US-09-835-976B-94	Sequence 94, Appl
26	162.4	3.8	712	11	US-09-835-976B-17	Sequence 17, Appl
27	162.2	3.8	424	10	US-09-960-352-9340	Sequence 9340, Ap
28	135.4	3.2	359	11	US-09-835-976B-91	Sequence 91, Appl
29	134.8	3.2	274	11	US-09-835-976B-109	Sequence 109, App
30	134.8	3.2	342	11	US-09-835-976B-88	Sequence 88, Appl
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33	121.4	2.8	251	11	US-09-835-976B-101	Sequence 101, App
34	120.4	2.8	503	11	US-09-835-976B-49	Sequence 49, Appl
35	118	2.8	242	11	US-09-835-976B-26	Sequence 26, Appl
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37	110	2.6	235	11	US-09-835-976B-107	Sequence 107, App
38	110	2.6	272	11	US-09-835-976B-57	Sequence 57, Appl
39	107.8	2.5	313	11	US-09-835-976B-102	Sequence 102, App
40	107	2.5	196	11	US-09-835-976B-37	Sequence 37, Appl
41	105.4	2.5	372	11	US-09-835-976B-78	Sequence 78, Appl
42	105	2.5	365	11	US-09-835-976B-53	Sequence 53, Appl
43	103.4	2.4	255	11	US-09-835-976B-100	Sequence 100, App
44	103.2	2.4	250	11	US-09-835-976B-95	Sequence 95, Appl
45	101.6	2.4	175	11	US-09-835-976B-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1

US-09-835-976B-15
; Sequence 15, Application US/09835976B
; Publication No. US20030027983A1
; GENERAL INFORMATION:
; APPLICANT: Mount, David B.
; APPLICANT: Delpire, Eric
; APPLICANT: Gamba, Gerardo
; APPLICANT: Alfred L. George, Jr.
; TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC AC
; TITLE OF INVENTION: POLYPEPTIDES AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. US20030027983A1 1242-26-2
; CURRENT APPLICATION NUMBER: US/09/835,976B
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 4260
; TYPE: DNA
; ORGANISM: Homo sapiens
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; NAME/KEY: CDS
; LOCATION: (165)..(3614)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (267)
; OTHER INFORMATION: n=c or a, Xaa=Leu or Ile
; NAME/KEY: misc feature
; LOCATION: (1200)
; OTHER INFORMATION: n=c or a, Xaa=Leu or Ile
; NAME/KEY: misc feature
; LOCATION: (2529)
; OTHER INFORMATION: n=c or a, Xaa=Leu or Ile
US-09-835-976B-15

Query Match 99.9%; Score 4257; DB 11; Length 4260;

Best Local Similarity 100.0%; Pred. No. 0; Matches 4260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	61	TGTTATTTTCAAGTTATCTTTGTATTCAGTCAAAAGTAGCTAGCGTAAGAGGAAGAT	120
QY	121	TTTGGAGGTTCCCCCACTTTTGTGTTTCTTAAAGAAACAAATGCATCTCCAGAAA	180
DB	121	TTTGGAGGTTCCCCCACTTTTGTGTTTCTTAAAGAAACAAATGCATCTCCAGAAA	180
QY	181	CCACCAACCAAGTGGCTTCAGTTCGGTTTCAATGGTACCCGACCAAGATTCGATGACATTC	240
DB	181	CCACCAACCAAGTGGCTTCAGTTCGGTTTCAATGGTACCCGACCAAGATTCGATGACATTC	240
QY	241	CAGGTTTGTGACACACAGTCCGGACNTCAGCTCTCGATCTAGTTCCTCCGAGTAAGATTTA	300
DB	241	CAGGTTTGTGACACACAGTCCGGACNTCAGCTCTCGATCTAGTTCCTCCGAGTAAGATTTA	300
QY	301	GCTCCGGGAAAGCGTGCCTGAAACAAAGCCGAGTGAGCTATGAGTGAGATGCTGGGG	360
DB	301	GCTCCGGGAAAGCGTGCCTGAAACAAAGCCGAGTGAGCTATGAGTGAGATGCTGGGG	360
QY	361	CCACCACTTCGCTGGCAACTGTGCACTGGATCCACCCAGTGACCGGACTTCTCACCCCC	420
DB	361	CCACCACTTCGCTGGCAACTGTGCACTGGATCCACCCAGTGACCGGACTTCTCACCCCC	420
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DB	481	AGACCGGACATGAAGAGCTCGAAATGCTTATCTCAATTAATTCCAATTAAGAAGGAG	540
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DB	781	TAGCCCTTACATGGGTGGGACACAGCTGGAGTCTCTCAGGCTTTTGCATTTGCTTTA	840
QY	841	TCGTGCTGCTGTA CAATTTGATGCTATCTCCATGATGTCATTCGCACATTAATGGAG	900
DB	841	TCGTGCTGCTGTA CAATTTGATGCTATCTCCATGATGTCATTCGCACATTAATGGAG	900
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DB	901	TGTTGACGCTGGGGCTCATCTTTATGATTTCCGGGCACTGGGGCCAGAGTTGGTG	960
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RESULT 2

US-09-835-976B-3

; Sequence 3, Application US/09835976B

; Publication No. US20030027983A1

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; GENERAL INFORMATION:
; APPLICANT: Mount, David B.
; APPLICANT: Delpire, Eric
; APPLICANT: Gamba, Gerardo
; APPLICANT: Alfred L. George, Jr.
; TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC AC
; TITLE OF INVENTION: POLYPEPTIDES AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket NO. US20030027983A1 1242-26-2
; CURRENT APPLICATION NUMBER: US/09/835,976B
; CURRENT FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 3
; LENGTH: 4215
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
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; OTHER INFORMATION: n=c or a, Xaa=Leu or Ile
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; US-09-835-976B-3

Query Match          97.2%; Score 4139.4; DB 11; Length 4215;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 4208; Conservative 0; Mismatches 5; Indels 47; Gaps 2;

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DB 2846 GCAGAGTGAAGTGTGGAGATGCACAGTGCATATCTGCTTATACATATGAGGCG 2905
QY 3135 ACTTTGATGTAAGCAAAAGTCTCCAGATGCTTCCGACATGCTGCGCTATCCAAACACAG 3194
DB 2906 ACCCTGATGTAAGCAGAGGTCCTCAGATGCTTCCGCAATGCTGCGCTCTCCAAACACAG 2965
QY 3195 CGAGACAGAGGCAAAATTTGGTGAAGACCGAACTCAATGCTACGATGACCAAGATT 3254
DB 2966 CGAGACAGGAGGCAAGCTGTTGAAAGTCAATGCTCAATGCTTCTTCTTCTTCTTCTTCTTCT 3025
QY 3255 GGCTCTGATGAGGAGAGACAGAACTTATCAGGAGAGGTCATGATGATGCTTGGCA 3314
DB 3026 GGCTCTGATGAGGAGAGACAGAACTTATCAGGAGAGGTCATGATGATGCTTGGCA 3085
QY 3315 AAAGCAAGTACATGTCATCTCCGGGACAAAAGCAAGTCAATGGAAGGATTTCCAGGAC 3374
DB 3086 AAGGATAAATACATGTCATCTCCGGGACAAAAGGTCATGTCATGGAAGGATTTCCAGGAC 3145
QY 3375 CTGCTTAACATGCTCCGACCAAGTCCCAATTTGTAGGCGGATGTCATACAGCAGTGAACCTC 3434

Db 3146 CTACTTAATATCGTCCGACAGCTCCAAAGTGAAGAGTGCATACAGCAGTGAAGTCT 3205
Qy 3435 AACGAGTTATAGTTAAAGTCCCATGAAGCAAGCTGTTTATTGAATATGCCAGG 3494
Db 3206 AATGAAGTTATAGTCAACAGTCTCATGAAGCAAGCTGTTTATTGAATATGCCAGG 3265
Qy 3495 CCACCCCGAAACCTCGAGGATGATGAAATACATACAGTCTCTAGAGTGTCTTACCGAG 3554
Db 3266 CCACCCCGAAACCTCGAGGATGATGAAATACATACAGTCTCTAGAGTGTCTTACCGAG 3325
Qy 3555 GGACTAGACGAGTCTTCTGTCGGGTGTGGCAGTGAAGTGAATACCATTTATTTCA 3614
Db 3326 GGATTAGACGAGTCTTCTGTCGGGTGTGGCAGTGAAGTGAATACCATTTATTTCA 3385
Qy 3615 TTAACCTACTCTAATGACCGTCTGACCTGTTTCTTAAAGGCTAGTCTCTCATGG 3674
Db 3386 TAATCAGCTGTGGGAGTTCTGCGTGTCCGACTTCCCTAA---GACTCATCGTCCATGG 3442
Qy 3675 AAGTGCAGCTCAATTACTACCACTCCCACTCAACTAGAGCCTGTGTTCTGTACACATCA 3734
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Qy 3735 TACTGAACCTCTTATGAGCTGAGCTTCAAGTACCTGTGTAAAGAGCTCCCATCTGATCT 3794
Db 3474 -----TATTTCTGAGAGCTGAGCCCATCTATGCTCTT-----GGCTGCAACATGATCT 3523
Qy 3795 GCAGTCAATTACGAAAGCAATATTCCTCAACATCAGAACATGCTCAAGTCTTTCA 3854
Db 3524 GC---CATCCAGCAGAAACAAATAATCCCTCAA---CAGAAGAATGGTCAAGTCTTAAA 3577
Qy 3855 AGCCACTGCTGAGCAGTCAAGGCAAAATAGAAATTAACAAGCTGAGCCAA----- 3905
Db 3578 AGCTATTTCTATGCGAGGAGAGGCAAGTCAAAATTTAACAGCTAAGCCAAAGGNAACCT 3637
Qy 3906 -----TAAATGAATGGTAAAGGGATGCTAGAAATTTCAACTGAAGAAA 3950
Db 3638 TTGGCACACAGAAGGTAATAGTTAGTTAGTAAACATATGCTAGAAATGTAAGTGGCAACAG 3697
Qy 3951 AAAGCAAGTCAAGTATTCAGCAATTAAGATGATCTCAGAGTCAAGTCTCAATGT 4010
Db 3698 AAAGCA---ATGTTTATATCTAACATTCAGGACGAGTTTTCAGAGACACGGGTCAAGTGA 3753
Qy 4011 TGAC 4014
Db 3754 GCAC 3757

RESULT 6

US-09-917-800A-1667
; Sequence 1667. Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22

; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1667
; LENGTH: 3726
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_0192229
US-09-917-800A-1667

Query Match 39.3%; Score 1674; DB 10; Length 3726;
Best Local Similarity 71.6%; Pred. No. 0;
Matches 2212; Conservative 0; Mismatches 872; Indels 6; Gaps 1;

Qy 536 AGGATGAAATATTTTGATAAAATTTGGCACTCTTTGAGGAAGAAATGGACACAGACC 595
Db 171 AGGAAATGACTACTATGACCGGAACCTGGCACTGTTTGGAGGAGCTGGACATCCGCC 230
Qy 596 GAAGGTGCTTCCCTCCTCAACCGCATGCGCAATTTACACTAATCTGACTCAAGGAGCAAA 655
Db 231 AAAGGTATCATCTCTCTGGGCAAGCTTGTGAGTATACCACTTCCCAAGGAGCCNA 290
Qy 656 GGAAATGAAGAGGAGCAAAATCATCCTGAAAGGGAAGAAAGCCCAACCAAGACCCCCA 715
Db 291 GGAGCAGCAGGAAGCTGAGAGTGGAGAGGTGGCCGTCGGAGAGCGCCCAAGGCCACCA 350
Qy 716 AATGGTACCTTTCATGGGTGCTACCTCCCATGTCTACAAATATTTTGGAGTATCTCT 775
Db 351 CATGGCACCTTATGGGAGTGTACCTGCCCTCGCCTGCAGAAATATCTTCGGGGTCTATCT 410
Qy 776 TTTTTCACGCTTACATGGGTGGGCGACAGCTGAGTCTTTCAGGCTTTTGGCAATGT 835
Db 411 CTCTCGGGCTGACCTGGATGGTGGGCGACAGCTGGCGTGTGCGAGGCTCTCTCATGT 470
Qy 836 CTTATCTGCTGCTGTACAAATGTTGACTGTATCTTCCATGAGTGCCATTTGCCACTAA 895
Db 471 CCTCATCTGTTGCTGTCTGCTGCTGACAGCCATCTCCATGAGTGCCATGCCACCAA 530
Qy 896 TGGAGTGTGCCAGCTGGGGGTCTACTTTATGATTTTCCCGGCGACTGGGGCCAGATT 955
Db 531 TGGTGTGGTTCAGCTGGTGGCTTTACTTTCATGATTTTCCGCTCTTTGGGACCAAGATT 590
Qy 956 TGGTGGGCTGTGGGCTCTGCTTTTATCTTGGTACCACATTTGAGAGCCATGTACAT 1015
Db 591 CGGAGTGTGTGGGCTTATGCTTCTACCTGGGAGCCACATTTGAGAGCCATGTATAT 650
Qy 1016 CTTTGGTGCATTTGAAATCTTTTCTGGTCTATATCTGCTCCCGGAGTGGCATTTTCACAG 1075
Db 651 CTAGAGCCATTTGAGATCTTGTCTGACCTACATGCTCCACAGCTGCCATCTTTTACCC 710
Qy 1076 TGATGACGACTCAAGGAATACAGCCATGCTAAATTAACATGCTGTGTCTAGGACAGC 1135
Db 711 ATCGGGCACACAGCATGTCAAGCGCCACCTTGAATAACATGCGGGGTGTACGGAACCA 770
Qy 1136 TTTCTTGGTCTTATGTTATAGTGTATTTATCGGCTGACCTATGTGAACAAGTTTCC 1195
Db 771 TTTCTGACTTTTCATGACCCCTAGTGGTGTGTCGGTGTCAAGTATGTGAACAAGTTTCC 830
Qy 1196 CTCANTTTTCTGGCTGTGTCTATTTGCTTCCATCTTTGGCCATCTATGCTGGAGCCATCA 1255
Db 831 CTCACCTTCTCGGCTGTGTGATCATCTCCATCTCTCCATTTTACGTGGGAGGATCAA 890
Qy 1256 GTCTCTTTTGTCTCTCAACATTCGCGGTGTGATGTGGGTAAACCGCACTCTTTTCATC 1315
Db 891 GTCCCGCTTTTGACCCCTCTCTGTTTTCGCGGTGTGATGTGGGCAATAGGACTCTGTCTCG 950

1316 AAGACACATTGAGCTTGGCTCTAAGACCAAGGAATTAACAACATGACAGTCCCATCAA 1375
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951 GGACCAAGTTTGACATCTGTCGCAAGACAGTTGTGGTGGCAATAGACAGATGGCCACCG 1010
Qy |||||
1376 GTTATGGGATTTCTCTGTAACCTCGAGTCAATTTTTCATGCGCACTGTGATGAATACTT 1435
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1011 GCTGTGGACTTCTCTGCGCACAGCCCCAACCTTACTGTGACTCTGTGACCCCTACTT 1070
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1071 CCTGTCTCAACAATGTGACAGATTTCTTGGCATACCTGGGCAGCTGTGGTGTGCTCCA 1130
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1496 AGAGATCTTTGGAGTATTTACTACCCAGAGGAGAGATCATCGAAAGCCTTCAGCCNA 1555
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1251 CACATCTTACCGTGTGGTGGCATCTTTTCCCTCTGTGTAAACAGGCATCATGGCTGG 1310
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1670 ATCAACACAGATCTGGAGATCTGAAAGATGCTCAGAGTCTATTCCGATTTGGTACTATCCT 1729
Db |||||
1311 CTCNAACCGTTCGCGGGACCTCCGTCATGCTCAGAGTCTATCCCTGTGGGGACCATCTCT 1370
Qy |||||
1730 TGCCATCTGACACCTCTTGTGTATTTAAGCAATGTGTCTCTTTTGGTGTGATGTAT 1789
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1371 GGTATTTGTCACACATTCACCTGTGTACTTTCAGCAGTGTGATCTCTTCGGTGGCTGCA 1430
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1790 TGAAGGGTGTGTCTCAGAGACAAGTTCGGTGATGCTGTGAAGGTAAATTTGGTGGTAGG 1849
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Qy |||||
1850 CACTTATCTTGGCCATCCCATGGGTGATTTGTTATTTGGCTCTTCTTTTCAACATGTGG 1909
Db |||||
1491 CACTTGGCTGGCCCTTCACTTGGGTCTATCGTGGTTCGCTCTCTTCTTCAACATGTGG 1550
Qy |||||
1910 GCTGACCTTACAGCCTCACAGGTGACCGAGGCTGTACAGCTATTGGCCAAAGATAA 1969
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1551 TGCCGGCTTCAAGTCTCACTTGGGGCCACGTTTACTTGAAGCAATTTGCCAAGGATAA 1610
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1611 CATCATCCCTTCTCTCCGGTGTTTGGCCACCGGAAGCAATGGTGAAGCAACGTGGGC 1670
Qy |||||
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Db |||||
1671 CCTCTCTGACAGGGCTCATCGCTGAGCTGGGCATCTCTCATCGCTCTCCCTTGACATGCT 1730
Qy |||||
2090 GSCCCCAATTTCTTCCATGTTTTTCTCATGTGTTACCTCTTTGTAAACTTGGCATGTGC 2149
Db |||||
1731 GSCCCCAATTTCTTCCATGTTTTTCTCATGTGTTACCTCTTTGTAAACTTGGCATGTGC 1790
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1791 TGTGACAGACACTTCTGAGGACCCCAACTGGCGGCCCGGTTCAAGTACTATCACTGSGC 1850
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Db |||||
1911 CGCCCTTAGTGGCCATTTGGTATCTGCGAGGCATGATCTACAAGTACATCGAGTACCAGGGC 1970
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1971 TGAGAAAGATGGGTGATGGAATCCGAGGCTGTCTCTGAGTGGCGGCACGATATGCAT 2030

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2450 ACTGAAACTAGATGAAGACTTACATGTCAAGCATCTCGCTCTCTCCTCCTCCTCTGCTCACA 2509
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2510 GCTCAAAGCAGAAAGGTTNTACATTTTGTGGGCTCTCTCATCTGTGGGAACTTCTCTAGA 2569
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2151 ACTTAAGGCTGGAAAGGCTGACAACTGTTGGCTCTGTCTATCCAGGGCAGCTTCTGGA 2210
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2331 CATCCAGTCTTGGCGCTGGGTGGCATGAGACATAAATCCGTGGTGTGGGCTGGCCCTA 2390
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2930 GCTTATGCTACTACATTCCTACTGAAACACACAGTGTGGGAAAGTGCAGATAGC 2989
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2571 GCTGATGTGCTGCTCTCTGCTGCGCCAGCAAGGTTTTGGAAGAAAGTGCAGATGCG 2630
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Db 3111 CCTGTCTTACTGAACATCCCGGCCCTTAAGAACAGTGAGGGTGATGAGAACTACAT 3170
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Db 3171 GGAAATTCCTTTGAAGTCTTAACCGAGGCGCTTGAACGGGTGTTGTTGGTGGTGGTGG 3230
Qy 3590 CAGTGAAGTGATCACCAATTTATTCATAACC 3619
Db 3231 CCGGGAAGTCATCACCAATCTATCTTGAGC 3260

RESULT 7
US-09-835-976B-1
; Sequence 1, Application US/09835976B
; Publication No. US20030027983A1
; GENERAL INFORMATION:
; APPLICANT: Mount, David B.
; APPLICANT: Delpire, Eric
; APPLICANT: Gamba, Gerardo
; APPLICANT: Alfred L. George, Jr.
; TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC AC
; TITLE OF INVENTION: POLYPEPTIDES AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. US20030027983A1 1242-26-2
; CURRENT APPLICATION NUMBER: US/09/835,976B
; CURRENT FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 5239
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (5)..(3253)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (161)
; OTHER INFORMATION: n=a or c, Xaa=Leu or Ile
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (260)
; OTHER INFORMATION: n=a or t, Xaa=Leu or Ile
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3086)
; OTHER INFORMATION: n=a or c, Xaa=Leu or Ile
US-09-835-976B-1

Query Match 33.3%; Score 1418; DB 11; Length 5239;
Best Local Similarity 66.9%; Pred. No. 0;
Matches 2104; Conservative 0; Mismatches 1010; Indels 33; Gaps 5;

Qy 483 GACGGACATAAGAAAGCTCGAAATGTTATCTCAATAATTCCTCAATTTATGAAGAAGGAGAT 542
Db 131 GATGAAATCCAGAGAAACAGCCCATTCNTCAACAATGTCGAGGTGGAACAAGAGAGC 190
Qy 543 GAAATTTTGTATAAATTTGGCACTCTTTGAGGAAGAAATGACACAGACCGAAGGTG 602
Db 191 TTCTTTGAAGGGAAGAACATGGCACTTTTCGAGGAGGAGATGACAGTAAACCCCATGGTG 250
Qy 603 TCTTCCTCTCTCAACCGCATGGCAATTAACATTAATCTGACTCAAGGACAAAGGAACAT 662
Db 251 TCTCTGCTGNTCAAGCTGGCCAACTACCAACCTGAGCCAGGCGCTGGTGAGAC 310
Qy 663 GAAGAGGCGAAGAACTACTAGGGAAGAAAGAACCCCAAGACCCGCCCAATGGGT 722
Db 311 GAGGAGGACGAGAGAGCGCGGGCGGGA-----GGCCAAAGGCTCGCGCATGGGC 361
Qy 723 ACCTTCATGGGTGTCTACCTCCCATGTCTACAAAATATTTTGGAGTGATCCTTTTITA 782
Db 362 ACCTTCATGGGTGTCTACCTCCCATGTCTACAAAATATTTTGGAGTGATCCTTTCTCTG 421
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Qy 783 GGCCTTACATGGGTGGTGGGCACAGCTGGAGTCTTCTCAGGCTTTTGTCAATTTGTCTCTTATC 842
Db 422 GGCCTGAGTGGATCGTGGGGGTGGTGGTCTCTTGGAGTCTCTTCTCTCATCGTGGCCATG 481
Qy 843 TGCTGTCTCTGTACAATTTGACTGTATCTCCATGAGTGCATTTGCAACATTAATGAGGTG 902
Db 482 TGCTGCACATGTACAATGCTACCGCCATTTCCATGAGTGGCATCGCTACCAACGGTGTG 541
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Qy 963 GCTGTTGGCTCTGCTTTTATCTTGGTACCAACATTTTGACAGAGCCATGTACATCTCTTGT 1022
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Qy 1083 GCACCTCAAGGAATCAGCAGCCATGCTAAATACATGCGTGTCTAGCGGCACAGCTTTCTTGT 1142
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Qy 1143 GTCTCTTATGTTAGTGGTATTTTATCGCGCTACGCTATGTGAACAAAGTTTGCCTCANTT 1202
Db 782 GTGCTCATGGCCCTGGTGGTCTTCTGGGCGTCAAGTATGTCAACAAGCTGGCGTGGTC 841
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Qy 1263 TTTGCTCTCCACACTTCCCGGTCTGCATGCTGGGTACCGGCACCTTTTCATCAAGACAC 1322
Db 902 TTGACACCCCGGACATCCCGGTCTGCTCTGGGGAACCGCACGCTGTACGCGCGAGC 961
Qy 1323 ATTGACGTTTGTCTTAAGACCAAGGAAATTAACAACATGACAGTCCCATCAAAAGTTATGG 1382
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Qy 1383 GGATTTCTGTAACTCGAGTCAATTTTCAATGCCCACCTGTGATGAATATCTTTTTCAC 1442
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Qy 1503 CTTTGGAGTAATTAACCTACCAAGGAGAGATCATCGAAAA-----GCTTTCAGCC 1553
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Qy 1614 TCCTTACGCTTCTGGTGGAACTCTTCTTCCCTCTGTACAGGTATCATGGCTGATCA 1673
Db 1259 TCCTTACCCCTGCTGGTTGGCATCTACTTCCCTCCGTGACCGGTATCATGGCGGTTCA 1318
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Qy 1734 ATCTGACCACTCCTTTTGTATTAAGCAATGTTGTCTCTTTTGGTGCATGATGA 1793
Db 1379 ATAGTGACGAGCTCTTTTCTATCTCTCTGCAATTTGTCTGTTTGGGCGCTGCATGA 1438
Qy 1794 GGGGTGTTCTCAGAGACAAGTTCCGTGATCTGTGAAGGTAAATTTTGGTGTAGGAC 1853
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1854 QY TTATCTTGGCCATCCCATGGGTGATTGTTATTGGCTCCTTCTTTTCAACATGTGGGCT 1913
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1914 QY GGACTTCAGAGCTCAACAGTGCACGAGGCTGCTAACAGTATTGCGCAAGGATAACATC 1973
1559 Db GGCTTCAGACCTCTACGGGGGACCGCGCTTACTGCGGCTTACTGCGGCTTACGCGCTGACGSCATC 1618
1974 QY ATACCGTTTCTGAGGGTTTTTGGCCACACAGCAAAAGCCNATGGGGAACCTTACCTGGGCTTTA 2033
1619 Db GTCCCTTCTCTGAGGTGTTTGGCCACGGGAAGGCCAAGGGAGGCCACGTGGGCGTGT 1678
2034 QY CTTTAACTGCTGCCATTGCAGAGCTTGGAAATACTCATTTGCTCCTCGATCTTGTGGCC 2093
1679 Db CTGCTGACAGTCTCTATCTGCGAGACTGSCATCTCATCGCTCTCTGGAAGAGCTGGCC 1738
2094 QY CCAATCTTTTCATGTTTTTCTCATGTTTACCTCTTTTGTAAACTTGGCATGTGCTTTG 2153
1739 Db CCGATCTCTCCATGTTCTTCTCATGTGCTACTGTTCTGTAACCTGCGCTGCGCGTG 1798
2154 QY CAAACATTACTTGAACCCCACTGGAGACCCCGATTCCGCTACTACCATTTGGGCGCTT 2213
1799 Db CAGACCTGCTACTGTAACCCCACTGGCGTCCACGCTTCAAGTTTCTACCACTGGACCCCTG 1858
2214 QY TCTTTTCATGGGAATGAGTATCTGCTGGCTCTGATGTTTCATTTCTTCTGGTATTATGCC 2273
1859 Db TCTTTTCTGGGTATGAGCTGTGCTGGCGCTGATGTTTCATCTGCTCTGGTACTACGCG 1918
2274 QY ATTGTAGCCATGGTAAATAGCTGGTATGATCTCAAGTACATTGAAATACCAAGGAGCTGAG 2333
1919 Db CTGTCGGCATGCTCATGCTGGCTGATCTCAAGTACATCGAGTACCGCGGGGCGGAG 1978
2334 QY AAAGATGGGTGATGGTATCGTGGCTGCTCCTCAGTGCAGCGCGGTTCCTTTGCTT 2393
1979 Db AAGGAGTGGGGGATGGCATCGTGGCTTATCCCTGAACCGCGCGCTACGCTCGCTG 2038
2394 QY CGATTGGAGGAGGACCTCCACACTAAACTGGAGGCTCAGTGGCTGTTGTTATCTG 2453
2039 Db CGCTGGAGACGCTCCCCCCCCACCAAGAACTGGAGGCCCAAGTGTGTTGATGCTG 2098
2454 QY AAATAGATGAGACTTACATGTCAAGCATCTCGCCTCTCACCTTTGCTTCCCTCACAGCTC 2513
2099 Db AACCTGGAGCGGAGCAGCGCTGAAGCACCCCGCTGCTGTCTTCAAGTGGAGCTG 2158
2514 QY AAAGCAGAAAGGTTNCTATTTGTGGCTCTGTCATCGTGGGGAATCTTCTTAGAGAAC 2573
2159 Db AAGCGCGCAGGGGCTGACCATCTGTTGGCTCGTGGAGGAGCGTACCTGACACAAG 2218
2574 QY TACGGTGAAGCTTTAGCTGCTGAGCAGACCAATAAAGCACTTAATGGAGCAGAGAGGTA 2633
2219 Db CACATGGAGGCTCAGCGGGCCGAGGAGAACATACCGTCTCCCTTAATGAGCACAGAGAAGACC 2278
2634 QY AAAGATTCTGCGAGCTGTGTGGCGCGCAAGCTGAGAGGGGCAATTTCCACCTCATC 2693
2279 Db AAGGCTTCTGCCAGCTGTGTGCTCTGCTCCAGCTGCGGATGGCATGTCCACCTGATC 2338
2694 QY CAGTCATGTGGCTTTGGGGCATGAAGCACACACGGTGGTGAATGGGCTGGCCTAATGGC 2753
2339 Db CAGTCGGCGGCTGGCGGCTGAAGCACACACGGTGTCTCATGGCTGGCGCGCATCC 2398
2754 QY TGGCGTCAAGCGAGATGCCCGCTTGGAGACTTTTATTTGGCACAGTTCGAGTGACA 2813
2399 Db TGGAGCAGGAGGACAAACCTTCTCTGGAGAACTTTGTAGACACCGTCCGCGACACC 2458
2814 QY ACTGTCGCCATCTTTCAGCTGCTGTGTGCTAAACACATCTCTCTTTCCAGCAATGTG 2873
2459 Db ACCGCGCGCACCGGCTCTGCTGTGTGGCCAGAACGTCGACTGTGTTCCGAAACACAG 2518
2874 QY GAGCAATTTTCTGAGGCAACAATTGATGTGTGGTGAATTTGTCATGATGGGGGATGCTT 2933
2519 Db GAGCGCTTCGGCGGGGCGACATCGACGTTGTGTGATCGTGCACGACGGCGGATGCTC 2578
2934 QY ATGCTACTACCATTCCTACTGAAACAGCACAAAGGTGTGGCGGAAGTGCAGCATACGGATC 2993

2579 Db ATGCTGTGCCCTTCTCTGCTGGCCAGCACAAAGGTGTGGAGGAAGTGCAGTATGCGTATC 2638
2994 QY TTACAGTAGCCCAATTAGAAAGACAACAGTATCCAAATGAAGAAGGACCTTAGCCACTTTC 3053
2639 Db TTACCGTGGCCAGGTGGACGACAACAGCATCCAGATGAAGAAGGACCTTCAGATGTTTC 2698
3054 QY CTATATCACTTACCGATTGAGCGGAGGTAGAGTGGTGGAGATGCATGACAGTATATA 3113
2699 Db TTGTATCACTTGGCGATCAGCGCCGAGGTGGAGTGGTGGAGATGGTTGAAAACGACATA 2758
3114 QY TCAGCATATACTTACGAGCGCACTTTGATGATGGAACAAAGGTCCAGATGCTTCGGCAC 3173
2759 Db TCTGTTTTCACCTACGAGAGGACACTAATGATGGAGCAGAGTCCAGATGCTGAAGCAG 2818
3174 QY ATGCGGCTATCCAAAACAGAGCGAGACAGAGAGGCACAATTTGGTGAAGAAGCCGAAACTCA 3233
2819 Db ATGCACTGTCTCAAGAACGAGCAGGAGCGAGAGGCCAGCTGATCCACGACAGGAACACC 2878
3234 QY ATGTACGATTGACCAGCATTTGGCTCTGATGAGGACGAAGAGACAGAAACCTTATCAGGAG 3293
2879 Db GC-----GTCCACACCGCGCGCGCAGCCAGGACCCAAAGCGCCGCTACGCCAGAC 2929
3294 QY AAGGTGCACATGACTTTGGACAAAAGACAAAGTACATGSCATCCCGG---GGACAAAAGCG 3350
2930 Db AAGTGCAGATGACTTGGACCAGGAGAAAGTCTGATCGCTGAGAAAGTACAGGAGCAGAGAC 2989
3351 QY AAGTCAATGGAAGGATTCAGGACCTGTTAAACATGCGTCCGGACCACTCCAAATGTGAGG 3410
2990 Db ACCAGCTTATCCGGTTTCAAGACCTCTTTCAGCATGAAGCCGACCACTCCCACTCAGG 3049
3411 QY CGGATGCATACAGCAGTGAATACTCAACAGAGTTTATAGTTAAAGTCCCTCAAGCAAG 3470
3050 Db CGGATGCACAGGCTGTGAAGCTCAATGGCTGCTGTCNTCAACAGTCCAGGATCGCGAG 3109
3471 QY CTGTTTTTATGAATATGCCAGGGCCACCCCGAACCTTGAGGTTGATGAAGAACTACATG 3530
3110 Db CTGTCCTGCTCAACATGCCAGGTCCTCCCAAAAACCGGAGGGAGACGAGAACTACATG 3169
3531 QY GAGTTCCTAGAGGTGCTTTACCGAGGGACTAGAGGGAGTCTTACTTGTCCGGGTGGTGGC 3590
3170 Db GAGTTCCTTGAAGTCTGACCGCGGGCTGAACAGAGTCTCTCTGTCAGGGTGGCGGC 3229
3591 QY AGTGAAGTATCACAATTTATTATATA 3617
3230 Db CGGAGGTGATCACCATCTACTCTATA 3256

RESULT 8

US-09-835-976B-13
; Sequence 13, Application US/09835976B
; Publication No. US20030027983A1

GENERAL INFORMATION:

; APPLICANT: Mount, David B.
; APPLICANT: Delpire, Eric
; APPLICANT: Gamba, Gerardo
; APPLICANT: Alfred L. George, Jr.
; TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC AC
; TITLE OF INVENTION: POLYPEPTIDES AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney docket No. US20030027983A1 1242-26-2
; CURRENT APPLICATION NUMBER: US/09/835,976B
; CURRENT FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 13
; LENGTH: 5155
; TYPE: DNA

; ORGANISM: mouse
; FEATURE:

; NAME/KEY: CDS
; LOCATION: (73)..(3321)

; FEATURE:


```
Db 1952 TCGCGCTGATGTTTCATCTCTCTGTTACTACGCCNTTTTGGCCATGCTCATTTGCCGGCT 2011
QY TGAATCTACAGTACATGTTGAATACCAAGGAGCTGAGAAAGAAATGGGGTGATGGTATCCGTTG 2358
Db 2012 GCATCTACAAAGTACATCGAGTACCGCGGGCTGAGAAGAGTGGGGGATGTCATCAGG 2071
QY GGCTGCTCCCTCAGTCAGCCCGGTTTGGTTTGGTTCCGATTGAGAGAGACCTCCACACA 2418
Db 2072 GCTGTGCTACCTGAATGTCGCCCCCTAGCCCTCTGCGTGTGGAACAATGGGCCCCCACATA 2131
QY CTAATAAATCGAGGGCTCAGTTGCTTGTATTACTGAAACTAGATGAAGACTTTACATGTCA 2478
Db 2132 CCAAGACTGAGGCCCCAGGTGTTGGTGTGATGCTGAACTGAACTCGAGAGAGTGTGTA 2191
QY AGATCTCTGCTCTCTCACTTTGCTCTCAGCTCAAGTCAAGAGCAAGAAAGTNTCACTATTG 2538
Db 2192 AGCACCCCGCTGCTGTCTTCACTCTCAGCTGAAAGCTGGCAAGGCGCTGACCATCG 2251
QY TGGGCTCTGTCTATCGTGGGGAATCTCTAGAGAACTACGGTGAAGCTTTAGCTGTGAGC 2598
Db 2252 TGGGATCTGTGTAGAGGCACTTACTTAGACAAGCATGTGAGGCGCCAGAGGGCTGAAG 2311
QY AGACCATAAAGCACCTAATGGAGGAGAGAAAGTAAAGGATTTGCGAGCTGGTGG 2658
Db 2312 AGAATATCCGGTCTCTGATGAGTGAGAGAAAGAGGGCTTCTGCCAGCTGGTGGTGT 2371
QY CGCCCAAGCTGAGAGAGGCACTTTCCCACTCATCCAGTCAATGTGGCTTTGGGGGCATGA 2718
Db 2372 CCTCAACCTCGAGATGGTGGTCCCACTCATCCAGTCCGCTGGCTCGTGGCATGA 2431
QY AGCAACAACCGTGTGATGGCTGGCTTAATGGCTGGGCTCAAGCGGAAGATGCCCGG 2778
Db 2432 AACACAACACTGCTCTCATGGCTGGCCAGAGGCTTGAAGAGGAGCAGATATCTTTCT 2491
QY CTGGAAGACTTTTATGSCAGTTTCGAGTGACAACTGCTGCCCATTTGCACTGCTGG 2838
Db 2492 CCTGGAAGAACTTTGTAGACAGTCCGTTGACACTACAGACACATCAGGCTTTGTTGG 2551
QY TGGCTTAAACATCTCTTTTCCAGCAATGTGGAGCAATTTTCTGAGGGCAACATTG 2898
Db 2552 TGGCAAGAACATTCACCTTATTTCCCAACAACCAAGAGCGCTTCAGCGAGGACATTG 2611
QY ATGTGTGTGATTTGTCATGATGGGGATGCTTATGCTACTACATTCCTACTGAAAC 2958
Db 2612 ATGTGTGTGATGTCGATGACGGGGCATCTCATGCTTCTGCCCCCTTTCTGTGCGCC 2671
QY AGCAAGGTGTGGGAAAGTGACGATACCGATCTTCACAGTAGCCCAATTAGAAGACA 3018
Db 2672 AGCAAGGTGTGGGAAAGTGCCGATGCGCATCTTCACTGTGGCCAGGTGGATGATA 2731
QY ACAGTATCCAAATGAAGAGACCTTAGCCACCTTCTTATCATCTTACCTTAGCGCATTTGAGCGG 3078
Db 2732 ACAGCATCCAGTGAAGAGGACCTGCGAGATGTTCTGTACCACTCAGGATCAGTGCGG 2791
QY AGGTAGAAGTGTGAGATGCAATGACAGTATATCAGCATATACCTTACAGCGCACTT 3138
Db 2792 AGGTGAGGTGTGAGATGTTGAAATGATATTTCCGCAATTCACCTATGAGAAGACGC 2851
QY TGATGATGAAACAAAGTCCAGATGCTTCCGACATCGGCTATCCAAACAGAGCGAG 3198
Db 2852 TAATGATGGAGCAGAGGTTCACAGATGCTGAAACAGATGCAATGCTGACGATTTGAGCGG 2911
QY ACAGAGGGCAAAATTTGGTGAAGACCCGAAACTCAATGCTACGATTTGACCAAGCATTTGCT 3258
Db 2912 AGAGAGAGGCCAGCTGATTCATGACAGGAACATGCACTCCATCCACAGCACTGTCTA 2971
QY CTGATGAGGACGAAGAGACAGAAACCTTATCAGGAGAGGTGCACATGCTTTGGACAAAG 3318
Db 2972 GAAACCAAGCCCCACCAACA-----CCGACAAAGTGCAGATGACATGGACGAAAG 3022
QY ACAAGTACATGGCATCC---CGGGACAAAGCGAAGTCAATGGAAGGATTCAGGAGCC 3375
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Db 3023 AGAAACTCATTTGCAGAGAAAACACAGGAACAAGGACACTGGCCCCATCAGGCTTCAAAGACC 3082
QY TGCTTAAACATCGTCCGGACCAAGTCCAATGTGAGCGGATGCATACAGCAGTGAAGACTCA 3435
Db 3083 TCTTCAGCCTAAAGCCGACCAAGTCCAACGTCAGGAGGATGCATACTGCTGTGAAGNTCA 3142
QY ACGAGGTATATAGTTTAAACAAGTCCCATGAAGCAAGCTGGTTTATTTGAATATGCCAGGCG 3495
Db 3143 ACGGCGTAGTTTCTCAACAAGTCCCAGGATGCCCAACTGGTCTGCTGTAATATGCCAGGCG 3202
QY CACCCGAAACCTTGAGGCTGATGAAACTACATGAGTTCCTAGAGGTTCCTAGAGGTTCCTGACGGAAG 3555
Db 3203 CCCCMAAAGTCCGACGAGGAGCAAGAACTACATGAGTTCCTGAGGTTCCTGACGGAAG 3262
QY GACTAGACGAGTCTCTACTTGTCCGGGTGGTGGCAGTGAAGTGAATGATACCACTTTATTCAT 3615
Db 3263 GGCTGAACAGGTCCTCTCTGTCAGGGGTGGTGGCCGAGAGTGCATCACCATCTACTCT 3322
QY 3616 AAC 3618
Db 3323 AAC 3325
```

RESULT 9

US-09-835-976B-11

; Sequence 11, Application US/09835976B

; Publication No. US20030027983A1

; GENERAL INFORMATION:

; APPLICANT: Mount, David B.

; APPLICANT: Delpire, Eric

; APPLICANT: Gamba, Gerardo

; APPLICANT: Alfred L. George, Jr.

; TITLE OF INVENTION: PURIFIED AND

; TITLE OF INVENTION: POLYPEPTIDES AND

; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME

; FILE REFERENCE: Attorney Docket No. US20030027983A1 1242-26-2

; CURRENT APPLICATION NUMBER: US/09/835,976B

; CURRENT FILING DATE: 2001-04-16

; NUMBER OF SEQ ID NOS: 131

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11

; LENGTH: 5907

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(3348)

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (358)

; OTHER INFORMATION: n=c or a, Xaa=Leu or Ile

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1072)

; OTHER INFORMATION: n=c or a, Xaa=Leu or Ile

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (2746)

; OTHER INFORMATION: n=c or a, Xaa=Leu or Ile

; US-09-835-976B-11

Query Match

Best Local Similarity 32.7%; Score 1392.4; DB 11; Length 5907;

Matches 1917; Conservative 0; Mismatches 821; Indels 15; Gaps 2;

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QY 483 GACGACATGAAGAGCTCGAAATGCTTATCTCAATTAATTCCAATTATGAAGAGGAGAT 542
Db 55 GATGGCAACCCCAAGGAAAGCAGTCCCTTCATCAACAGCACCGACACAGAGGGAAG 114
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QY 543 GAATATTTTGTATATAAATTTGGCACTCTTTGAGGAGAAATGGACACAGACCGAAGGTG 602
Db 115 GAGTATGATGGCAAGAACATGGGCTTGTGTTGAGGAGGAGATGGACACAGCCCTATGGTG 174
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Db 2332 AACTGGCCGACGAGAAAGATCATCAGACGTGGAGAACTTCATTGAGCTGCTCCGGNA 2391
QY 2811 ACAACTGTGCCCATCTTGCATCTGTGGTGTAAACATCTCTTCTTTCCAGCAAT 2870
Db 2392 ACCACAGCTGGCCACTTAGCCCTCTGTGTGTACCAAGAACTTCCATGTTTCTGGGAAC 2451
QY 2871 GTGGAGCAATTTCTGAGGGCAACATTGATGTGTGGTGAATTTGTCATGATGGGGGATG 2930
Db 2452 CCTGAGCGCTTCTCTGAGGGCAGCATCGACGTTTGTGGATTTGTGCACGATGGAGGCATG 2511
QY 2931 CTTATGTCTACTACCATTCCTCTACTGAAACAGCAAGGTGTGGCAAAAGTGCAAGCATACGG 2990
Db 2512 CTCATGCTGCTGCCCTTCTCTGCTGGCCACCAAGGTCTGGGGAAGTGCAAGTGCCT 2571
QY 2991 ATCTTCACAGTAGCCCAATTAGAAGACAAAGATATCCAAATGAAGAAGCACTAGCCACC 3050
Db 2572 ATCTTCACGTGTGCCCGACATGATGACAAATAGATCCAGATGAAGAAGGATCTGACCACA 2631
QY 3051 TTCTTATATCACTTACGCAATGAGCGGAGGTAGAAGTGGTGAGATGCATCAGATGAT 3110
Db 2632 TTCTGTATCATTTACGCACTACTCGGAGGTGCGAGGTGGAGATGCATGAGCGGAC 2691
QY 3111 ATATCAGCATATACTTACGAGCGCACTTTGATGATGGAACAAAGGTCCAGATGCTTCGG 3170
Db 2692 ATCTCAGCTTACCTATGAGAGACGTTGGTGTAGGACGCGTTCCAGATGTCATA 2751
QY 3171 CACATGCGGCTATCCAAACAGAGCGGAGACAGAGAGGCAAAATGGTGAAGA 3223
Db 2752 CAGATGCAITTAACCAAGATGAGCGGAGCGGAGATCCAGAGTATCACAGA 2804

RESULT 10
US-09-835-976B-110
; Sequence 110, Application US/09835976B
; Publication No. US20030027983A1
; GENERAL INFORMATION:
; APPLICANT: Mount, David B.
; APPLICANT: Delpire, Eric
; APPLICANT: Gamba, Gerardo
; APPLICANT: Alfred L. George, Jr.
; TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC AC
; TITLE OF INVENTION: POLYPEPTIDES AND
; FILE REFERENCE: Attorney Docket No. US20030027983A1 1242-26-2
; CURRENT FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-835-976B-110

Query Match 17.3%; Score 735; DB 11; Length 807;
Best Local Similarity 100.0%; Pred. No. 5.7e-204;
Matches 735; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3526 ACATGGAGTCTCAGAGGTCTTACCAGCGGACTAGAGCGACTCTACTTGTCCGGGTG 3585
Db 73 ACATGGAGTCTCAGAGGTCTTACCAGCGGACTAGAGCGAGTCTACTTGTCCGGGTG 132
QY 3586 GTGGCAGTGAAGTGATCACCATTATTTCATACCTACTCTGAATGACCGTGTTCACCTG 3645
Db 133 GTGGCAGTGAAGTGATCACCATTATTTCATACCTACTCTGAATGACCGTGTTCACCTG 192
QY 3646 TTTTCTTAAAGCCCTACTCTCTCCATGAAGTGCAGCTCATTTACTTACCCTCCACTC 3705
Db 193 TTTTCTTAAAGCCCTACTCTCTCCATGAAGTGCAGCTCATTTACTTACCCTCCACTC 252
QY 3706 ACTAGAGCCCTGTGTTCTGTACATCATCATCTACTGACTCTTATGAGCTGAGCCCTCAAGT 3765
Db 253 AACTAGAGCCCTGTGTTCTGTACATCATCATCTACTGAACTCTTGTATGAGCTGAGCCCTCAAGT 312
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QY 3766 ACCTGTGTAAAGAGCTCCCATCTGATCTGCAGTCAATTACAGAAAAAGCAAAATATTCCCT 3825
Db 313 ACCTGTGTAAAGAGCTCCCATCTGATCTGCAGTCAATTACAGAAAAAGCAAAATATTCCCT 372
QY 3826 CAACATCAGAAACAATGCTCAAGTCTTTCAAGCCACTGTCTGAGCAGTCAAGGCAAAATTA 3885
Db 373 CAACATCAGAAACAATGCTCAAGTCTTTCAAGCCACTGTCTGAGCAGTCAAGGCAAAATTA 432
QY 3886 GAATTTAAACAAGCTGAGCCAAATAAATGAATTTGGTAAAAGGGATGCTAGAAATTTCAACTGAA 3945
Db 433 GAATTTAAACAAGCTGAGCCAAATAAATGAATTTGGTAAAAGGGATGCTAGAAATTTCAACTGAA 492
QY 3946 GAAAAAAGCAAGTCAAGTACGTATTTCAGCAATTAAGATGAATCTCAGAAAGTCATGGTTC 4005
Db 493 GAAAAAAGCAAGTCAAGTACGTATTTCAGCAATTAAGATGAATCTCAGAAAGTCATGGTTC 552
QY 4006 AATGTTGACACTGTGAGGATAACAACACTAGACAGCTTTCATCTTACTAAAGAAATTTATGG 4065
Db 553 AATGTTGACACTGTGAGGATAACAACACTAGACAGCTTTCATCTTACTAAAGAAATTTATGG 612
QY 4066 TCAAGTATATTTGGACCTATTATCTCGGCAAGCAAGATGCAACATTTTTCAGCTATA 4125
Db 613 TCAAGTATATTTGGACCTATTATCTCGGCAAGCAAGATGCAACATTTTTCAGCTATA 672
QY 4126 TTTCTTTAGTATACCCACTGCTGTAATTTTATATTTAGGATATACTTGAACATGGCTG 4185
Db 673 TTTCTTTAGTATACCCACTGCTGTAATTTTATATTTAGGATATACTTGAACATGGCTG 732
QY 4186 CAGCTCTACTTCTTCAAAAACATCCCCCAAAATACCAGATTTAAATATCCAAAAAAA 4245
Db 733 CAGCTCTACTTCTTCAAAAACATCCCCCAAAATACCAGATTTAAATATCCAAAAAAA 792
QY 4246 AAAAAAATAAAAAA 4260
Db 793 AAAAAAATAAAAAA 807
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RESULT 11

```
US-09-835-976B-112
; Sequence 112, Application US/09835976B
; Publication No. US20030027983A1
; GENERAL INFORMATION:
; APPLICANT: Mount, David B.
; APPLICANT: Delpire, Eric
; APPLICANT: Gamba, Gerardo
; APPLICANT: Alfred L. George, Jr.
; TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC AC
; TITLE OF INVENTION: POLYPEPTIDES AND
; FILE REFERENCE: Attorney Docket No. US20030027983A1 1242-26-2
; CURRENT FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 2290
; TYPE: DNA
; ORGANISM: Xenopus laevis
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: n=a, c, g, or t
US-09-835-976B-112
```

```
Query Match 14.4%; Score 613.4; DB 11; Length 2290;
Best Local Similarity 73.0%; Pred. No. 5.3e-168;
Matches 788; Conservative 0; Mismatches 291; Indels 0; Gaps 0;

QY 2538 GTGGCTCTGTCATCGGGGAACCTCCTACAGAACTACGGTGAAGCTTTAGCTGCTCAG 2597
Db 7 GAGGCAAGTACTTCTGGGAGACTACCTAGACAGCCATGACAGTACAGGACAGAG 66
```


NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-835-976B-84

Query Match 10.2%; Score 434; DB 11; Length 489;

Best Local Similarity 99.8%; Pred. No. 6.3e-116;
Matches 434; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCAGTAGAAGTATCTTAGTTCGGGCTTTTCTGCTGGTGAATCAAGGTATTGAAATG 60
DB 1 TCAGTAGAAGTATCTTAGTTCGGGCTTTTCTGCTGGTGAATCAAGGTATTGAAATG 60
QY 61 TGTATTTTCAAGTTATCTTTTGTATTCAGTCAAAAGTAGCTAGCGTAAGAGGAAGAT 120
DB 61 TGTATTTTCAAGTTATCTTTTGTATTCAGTCAAAAGTAGCTAGCGTAAGAGGAAGAT 120
QY 121 TTTCGAGGTTCCCGCCACTTTTGTGTTCTTAAAGAAACAAAATGCATCTCCAGAAA 180
DB 121 TTTCGAGGTTCCCGCCACTTTTGTGTTCTTAAAGAAACAAAATGCATCTCCAGAAA 180
QY 181 CCACCACCAAGATGCTTCAGTTCGGTTCATGGTGACACCGACAAAGATCGATGATTC 240
DB 181 CCACCACCAAGATGCTTCAGTTCGGTTCATGGTGACACCGACAAAGATCGATGATTC 240
QY 241 CAGGTTTGTGACACACAGTCGGACNTCAGCTCTCGATCTAGTTCCTCCGAGTAAGATTTA 300
DB 241 CAGGTTTGTGACACACAGTCGGACNTCAGCTCTCGATCTAGTTCCTCCGAGTAAGATTTA 300
QY 301 GCTCCCGGAAAGCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 301 GCTCCCGGAAAGCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 361 CCACCACCTTCGCTGCACTGTTGCACTGGATCCACCGACCGGACTTCTCACCCCC 420
DB 361 CCACCACCTTCGCTGCACTGTTGCACTGGATCCACCGACCGGACTTCTCACCCCC 420
QY 421 AGGATGTCATCGAGG 435
DB 421 AGGATGTCATCGAGG 435

RESULT 14

US-09-835-976B-18

; Sequence 18, Application US/09835976B

; Publication No. US20030027983A1

; GENERAL INFORMATION:

; APPLICANT: Mount, David B.

; APPLICANT: Delpire, Eric

; APPLICANT: Gamba, Gerardo

; APPLICANT: Alfred L. George, Jr.

; TITLE OF INVENTION: PURIFIED AND

; TITLE OF INVENTION: POLYPEPTIDES AND

; FILE REFERENCE: THERAPEUTIC AND SCREENING METHODS USING SAME

; CURRENT APPLICATION NUMBER: US/09/835,976B

; CURRENT FILING DATE: 2001-04-16

; NUMBER OF SEQ ID NOS: 131

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 18

; LENGTH: 1014

; TYPE: DNA

; ORGANISM: mouse

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (525)

; OTHER INFORMATION: n=a, c, g, or t

US-09-835-976B-18

Query Match 6.2%; Score 262; DB 11; Length 1014;

Best Local Similarity 78.3%; Pred. No. 2.7e-65;
Matches 342; Conservative 0; Mismatches 86; Indels 9; Gaps 2;

QY 5 TAGAAGTATCTTAGTTCGGGCTTTTCTGCTGGTGAATCAAGGTATTGAAATGTTT 64
DB 580 TACACGGATTCTTAATGGGCC--TTTGTGGCTGTAANTCAGGTAATTGAGGGTTTTT 637
QY 65 ATTTTTCAAAGTTATCTTTTGTATTGCACTCAAAAGTAGCTAGCGTAAGAGGAAGTTTG 124
DB 638 GGTTTTTTTCCTCTTATTTTGGCAATCAGAAGTAGCTAGTGTAGGAGGAAGAGTTTTT 697
QY 125 CGAGGTTCCCGCCACTTTTGTGTTCTTAAAGAA-----CAAATGCACTCTCCAG 177
DB 698 TGTGAGCTTTTCTTTTCTTTGTCAAAAAGGAGGGGGGGAATGCAATCCACCAG 757
QY 178 AAACACCAACCAAGATGCTTCAGTTCGGTTCATGGTGACACCGACAAAGATCGATGACA 237
DB 758 AAGCCACCAACCAAGATGCTTCAGTTCGGTTCATGGTGACACCAACTAAGATTGATGACA 817
QY 238 TTCCAGGTTTGTGACACACAGTCGGACNTCAGCTCTCGATCTAGTTCCTCCGAGTAAGAT 297
DB 818 TTCCAGGTTTGTGACACACAGTCGGACNTCAGCTCTCGATCTAGTTCCTCCGAGTAAGAT 877
QY 298 TTAGCTCCCGGAAAGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 357
DB 878 TTAGCTCCCGGAAAGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 937
QY 358 GGGCCACCACTTCGCTGGCAACTGTTGCACTGGATCCACCCAGTGACCGGACTTCTCACC 417
DB 938 GGGCTACTACTTCTCTGCAACTGTTGCCCTAGATCCTTCCAGTGACCGGACTTCTAATC 997
QY 418 CCCAGGATGTCATCGAG 434
DB 998 CCCAGGATGTTACGGAG 1014

RESULT 15

US-09-835-976B-92

; Sequence 92, Application US/09835976B

; Publication No. US20030027983A1

; GENERAL INFORMATION:

; APPLICANT: Mount, David B.

; APPLICANT: Delpire, Eric

; APPLICANT: Gamba, Gerardo

; APPLICANT: Alfred L. George, Jr.

; TITLE OF INVENTION: PURIFIED AND

; TITLE OF INVENTION: POLYPEPTIDES AND

; FILE REFERENCE: THERAPEUTIC AND SCREENING METHODS USING SAME

; CURRENT APPLICATION NUMBER: US/09/835,976B

; CURRENT FILING DATE: 2001-04-16

; NUMBER OF SEQ ID NOS: 131

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 92

; LENGTH: 402

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-835-976B-92

Query Match 5.8%; Score 245.8; DB 11; Length 402;

Best Local Similarity 96.9%; Pred. No. 7.7e-61;

Matches 250; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1026 ATTCGAAATCTTTCTGGTCTATATCGTCCCGAGCTGCCATCTTTTCAGTGATGACGCA 1085
DB 77 ATTTTACCTTAACAGGTTCTATATCGTCCCGAGCTGCCATCTTTTCAGTGATGACGCA 136
QY 1086 CTCGAAGGAATCAGCAGCCATGCTAAATAACATGCTGTCTACGGCACAGCTTTCTTGTC 1145
DB 137 CTCGAAGGAATCAGCAGCCATGCTAAATAACATGCTGTCTACGGCACAGCTTTCTTGTC 196
QY 1146 CTTATGTTATAGTGGTATTATTCGGGTATGATCGGTATGTAACAAGTTTGCCTCANTTTTT 1205

Db 197 CTTATGGTATTAGTGGTATTATTCGGCGTACGCTATGTGAACAAGTTTGCCTCACTTTTC 256
Qy 1206 CTGGCCTGTGTCATTGTGTCCATCTTGGCCATCTATGCTGGAGCCATCAAGTCTTCTTTT 1265
Db 257 CTGGCCTGTGTCATTGTGTCCATCTTGGCCATCTATGCTGGAGCCATCAAGTCTTCTTTT 316
Qy 1266 GCTCCTCCACACTTCCCG 1283
Db 317 GCTCCTCCACACTTCCCG 334

Search completed: November 27, 2003, 01:01:31
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